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OM protein - protein search, using sw model

Run on: October 8, 2004, 10:15:45 ; Search time 12 Seconds
(without alignments)
1466.643 Million cell updates/sec

Title: US-09-633-145-2
Perfect score: 1801
Sequence: 1 MFPCNNINISCVKNWNSND.....FGKIFQDSRRCKLFLELSS 338

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1801	100.0	339	1 TARI_HUMAN	Q96rj0 homo sapien
2	1757	97.6	338	1 TARI_MACMU	Q8hz64 macaca mula
3	1403	77.9	332	1 TARI_RAT	Q923y9 rattus norv
4	1351	75.0	332	1 TARI_MOUSE	Q923y8 rattus muscu
5	927.5	51.5	347	1 TAR2_RAT	Q923y7 rattus norv
6	815	45.3	306	1 GP58_HUMAN	Q9p1p5 homo sapien
7	813.5	45.2	343	1 GP57_HUMAN	Q9p1p4 homo sapien
8	782	43.4	338	1 TAR3_RAT	Q923y6 rattus norv
9	743	41.3	348	1 TAR3_HUMAN	Q96r19 homo sapien
10	741	41.1	333	1 TAR2_RAT	Q923x8 rattus norv
11	733	40.7	344	1 TAR7_RAT	Q923y3 rattus norv
12	732	40.6	345	1 TAR4_RAT	Q923y5 rattus norv
13	731	40.6	344	1 TAR1_RAT	Q923x9 rattus norv
14	730	40.5	344	1 TAR0_RAT	Q923y0 rattus norv
15	722	40.1	358	1 TAR4_RAT	Q923x5 rattus norv
16	722	40.1	358	1 TAR5_RAT	Q923x6 rattus norv
17	715	39.7	345	1 TAR6_HUMAN	Q96r18 homo sapien
18	713	39.6	358	1 TAR8_RAT	Q923y2 rattus norv
19	710	39.4	358	1 TAR9_RAT	Q923y1 rattus norv
20	704	39.1	358	1 TAR6_RAT	Q923y4 rattus norv
21	696	38.6	342	1 TAR5_HUMAN	Q969n4 homo sapien
22	679	37.7	362	1 TAR3_RAT	Q923x7 rattus norv
23	542.5	30.1	388	1 SH4_CAVPO	O70528 cavia porce
24	539	29.9	388	1 SH4_MOUSE	P97288 mus muscu
25	534	29.7	388	1 SH4_HUMAN	Q13639 homo sapien
26	529	29.4	406	1 SH4_RAT	Q62758 rattus norv
27	510.5	28.3	459	1 D1DR_FUGRU	P53452 fugu rubrip
28	497.5	27.6	465	1 DCDR_XENLA	P42291 xenopus lae
29	493.5	27.4	363	1 D1DR_CARAU	P35406 carassius a
30	492.5	27.3	358	1 HH2R_MOUSE	P97292 mus muscu
31	486	27.0	358	1 HH2R_RAT	P25102 rattus norv
32	481	26.7	457	1 DDDR_XENLA	P42290 xenopus lae
33	480	26.7	451	1 DADR_XENLA	P42289 xenopus lae

RESULT 1	TARI_HUMAN	STANDARD;	PRT;	339 AA.
ID	TARI_HUMAN			
AC	Q96RJ0;			
DT	15-MAR-2004 (Rel. 43, Created)			
DT	15-MAR-2004 (Rel. 43, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Trace amine receptor 1 (Tar-1).			
GN	TAR1 OR TAL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21374364; PubMed=11459929;			
RA	Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,			
RA	Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,			
RA	Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,			
RA	Branchek T.A., Gerald C.			
RT	"Trace amines: Identification of a family of mammalian G protein-			
RT	coupled receptors."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21580335; PubMed=1173224;			
RA	Bunzow J.R., Sonders M.S., Artamangkul S., Harrison L.M., Zhang G.,			
RA	Quigley D.I., Darland T., Suchland K.L., Pasumamula S., Kennedy J.L.,			
RA	Olson S.B., Magenlis R.E., Amara S.G., Grandy D.K.;			
RT	"Amphetamine, 3,4-methylenedioxymethamphetamine, lysergic acid			
RT	diethylamide, and metabolites of the catecholamine neurotransmitters			
RT	are agonists of a rat trace amine receptor."			
RL	Mol. Pharmacol. 60:1181-1188(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Kopatz S.A., Aronstam R.S., Sharma S.V.;			
RT	"cDNA clones of human proteins involved in signal transduction			
RT	sequenced (NOV-2002) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.			
CC	Activated by endogenous trace amines as well as metabolites of the			
CC	biogenic amine neurotransmitters. Trace amines are biogenic amines			
CC	present in very low levels in mammalian tissues. Although some			
CC	trace amines have clearly defined roles as neurotransmitters in			
CC	invertebrates, the extent to which they function as true			
CC	neurotransmitters in vertebrates has remained speculative. Trace			
CC	amines are likely to be involved in a variety of physiological			
CC	functions that have yet to be fully understood. This receptor			
CC	seems to be mediated by the G(s)-class of G-proteins which			
CC	activate adenylyate cyclase.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- TISSUE SPECIFICITY: Detected in low levels in discrete regions			
CC	within the central nervous system and in several peripheral			
CC	tissues. Moderately expressed in stomach. Low levels in amygdala,			
CC	kidney, and lung, and small intestine. Trace amounts in cerebellum,			
CC	dorsal root ganglia, hippocampus, hypothalamus, liver, medulla,			

ALIGNMENTS

34	475	26.4	377	1	SH1D_RABIT	P49145 oryctolagus
35	474	26.3	377	1	SH1D_HUMAN	P28221 homo sapien
36	473	26.3	374	1	SH1D_RAT	P28565 rattus norv
37	472.5	26.2	359	1	HH2R_HUMAN	P25021 homo sapien
38	472.5	26.2	359	1	HH2R_PANTR	P60021 pan troglod
39	471	26.2	446	1	DADR_DIDMA	P42288 didelphis m
40	469	26.0	374	1	SH1D_MOUSE	O61224 mus muscu
41	467	25.9	446	1	DADR_PIG	P50130 sus scrofa
42	466.5	25.9	377	1	SH1D_CANFA	P11614 canis famil
43	466.5	25.9	386	1	D1DR_OREMO	P47800 oreochromis
44	462.5	25.7	463	1	D5DR_FUGRU	P53454 fugu rubrip
45	461.5	25.6	376	1	SH1D_CAVPO	Q60484 cavia porce

CC pancreas, pituitary, pontine reticular formation, prostate,
 CC skeletal muscle, and spleen.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 CC EMBL; AF380185; AAK71236.1; -
 CC EMBL; AF200627; AAG17112.1; -
 CC EMBL; AY180374; AAC22154.1; -
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCR_RHODOPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 46 1 (POTENTIAL).
 FT DOMAIN 47 59 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 60 80 2 (POTENTIAL).
 FT DOMAIN 81 98 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 99 119 3 (POTENTIAL).
 FT DOMAIN 120 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 157 4 (POTENTIAL).
 FT DOMAIN 158 188 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 189 209 5 (POTENTIAL).
 FT DOMAIN 210 252 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 253 273 6 (POTENTIAL).
 FT DOMAIN 274 287 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 288 308 7 (POTENTIAL).
 FT DOMAIN 309 339 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 96 182 BY SIMILARITY.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 339 AA; 39091 MW; 5E72FA61CEFA0E0 CRC64;

Query Match 100.0%; Score 1801; DB 1; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.1e-116;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNWSDVRASLSLVLIITLTVGNLIVIVSISHFKQLHTPTNWL 60
 DB 2 MPFCHNIINISCVKNNWSDVRASLSLVLIITLTVGNLIVIVSISHFKQLHTPTNWL 61
 QY 61 IHSMTAVDFLLGLCLAMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSFISIDR 120
 DB 62 IHSMTAVDFLLGLCLAMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSFISIDR 121
 QY 121 YVAVCDPLRYKAKNNILVICWIFISWSVPVAFGMIFLELNFKAEEIYKGVHCRGG 180
 DB 122 YVAVCDPLRYKAKNNILVICWIFISWSVPVAFGMIFLELNFKAEEIYKGVHCRGG 181
 QY 181 CSVFFSKISGLVTFMTSPYIPGIMLCVYRIYLIKAEQARLISDANQKLGLEMKNGI 240
 DB 182 CSVFFSKISGLVTFMTSPYIPGIMLCVYRIYLIKAEQARLISDANQKLGLEMKNGI 241
 QY 241 SOSKERRKAVTKIGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLVWFGYLNSTFNP 300
 DB 242 SOSKERRKAVTKIGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLVWFGYLNSTFNP 301
 QY 301 MYAFYPPWFRKALKMMLFGKIFQKDSRRCKLFLLESS 338
 DB 302 MYAFYPPWFRKALKMMLFGKIFQKDSRRCKLFLLESS 339

RESULT 2

TAR1_MACMU

ID TAR1_MACMU STANDARD; PRT; 338 AA.
 AC Q8HZ64;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Trace amine receptor 1 (Tar-1).
 GN TAR1 OR TAL.
 OS Macaca mulatta (Rhesus macaque).
 OC Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miller G.M., Madras B.K.;
 RT "Cloning of trace amine receptor 1 (TAR1) from Rhesus monkey.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
 CC Activated by endogenous trace amines as well as metabolites of the
 CC biogenic amine neurotransmitters (By similarity). Trace amines are
 CC biogenic amines present in very low levels in mammalian tissues.
 CC Although some trace amines have clearly defined roles as
 CC neurotransmitters in invertebrates, the extent to which they
 CC function as true neurotransmitters in vertebrates has remained
 CC speculative. Trace amines are likely to be involved in a variety
 CC of physiological functions that have yet to be fully understood.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 CC EMBL; AY13366; AAN06172.1; -
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCR_RHODOPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 25 45 1 (POTENTIAL).
 FT DOMAIN 46 58 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 59 79 2 (POTENTIAL).
 FT DOMAIN 80 97 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 98 118 3 (POTENTIAL).
 FT DOMAIN 119 135 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 136 156 4 (POTENTIAL).
 FT DOMAIN 157 187 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 188 208 5 (POTENTIAL).
 FT DOMAIN 209 251 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 252 272 6 (POTENTIAL).
 FT DOMAIN 273 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 307 7 (POTENTIAL).
 FT DOMAIN 308 338 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 95 181 BY SIMILARITY.
 FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 338 AA; 38797 MW; 9E7B35456B409B CRC64;

Query Match 97.6%; Score 1757; DB 1; Length 338;
 Best Local Similarity 96.4%; Pred. No. 7.9e-113;
 Matches 326; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNNWSDVRASLSLVLIITLTVGNLIVIVSISHFKQLHTPTNWL 60

DB 1 MPFCHNIINISCVKNNWSDVRASLSLVLIITLTVGNLIVIVSISHFKQLHTPTNWL 60

QY 61 IHSMATVDFLLGCLVMPYMSVRSABHCWYFGEVFCCKIHTSTDMSSASIFHLSFISIDR 120
 Db 61 IHSMATVDFLLGCLVMPYMSVRSABHCWYFGEVFCCKIHTSTDMSSASIFHLSFISIDR 120
 QY 121 YVAVCDPLRYKAKMILVICVMIFISWSVPVAFAGMIFLELNFKAEEIYKHHVHCRGG 180
 Db 121 YVAVCDPLRYKAKMILVICVMIFISWSVPVAFAGMIFLELNFKAEEIYKHHVHCRGG 180
 QY 181 CSVFPSKISGVLTFTMTSPYIPGSMILCVYRIYLIJAKQARLISDANOKLQIGLEMKNGI 240
 Db 181 CSVFPSKISGVLTFTMTSPYIPGSMILCVYRIYLIJAKQARLISDANOKLQIGLEMKNGI 240
 QY 241 SOSKERKAVKTLGIYMGVFLICWCFFCTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 Db 241 SOSKERKAVKTLGIYMGVFLICWCFFCTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 QY 301 MYAFYFYPFRKALOMLFGKIFQKDSRCKLFLLESS 338
 Db 301 MYAFYFYPFRKALOMLFGKIFQKDSRCKLFLLESS 338
 RESULT 3
 TARI RAT
 ID TARI RAT STANDARD; PRT; 332 AA.
 AC Q92379; O8VHQ5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DE Trace amine receptor 1 (Tar-1).
 GN TARI OR TAL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI TaxID=10116;
 RN [1]
 RC STRAIN=Sprague-Dawley;
 RC MEDLINE=21374364; PubMed=11459929;
 RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
 RA Gogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
 RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
 RA Branchek T.A., Gerald C.;
 RA "Trace amines: Identification of a family of mammalian G protein-
 coupled receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum, and Pancreatic tumor;
 RC MEDLINE=21580235; PubMed=11723224;
 RA Bunzow J.R., Sonders M.S., Artamangkul S., Harrison L.M., Zhang G.,
 RA Quigley D.I., Darland T., Suchland K.L., Pasumamula S., Kennedy J.L.,
 RA Olson S.B., Magenis R.E., Anara S.G., Grandy D.K.;
 RA "Amphetamine, 3,4-methylenedioxymethamphetamine, lysergic acid
 diethylamide, and metabolites of the catecholamine neurotransmitters
 are agonists of a rat trace amine receptor.";
 RL Mol. Pharmacol. 60:1181-1188(2001).
 CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
 CC Activated by endogenous trace amines as well as metabolites of the
 CC biogenic amine neurotransmitters. Trace amines are biogenic amines
 CC present in very low levels in mammalian tissues. Although some
 CC trace amines have clearly defined roles as neurotransmitters in
 CC invertebrates, the extent to which they function as true
 CC neurotransmitters in vertebrates has remained speculative. Trace
 CC amines are likely to be involved in a variety of physiological
 CC functions that have yet to be fully understood. This receptor
 CC seems to be mediated by the G(s)-class of G-proteins which
 CC activate adenylate cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely distributed, but in low abundance,
 CC throughout the brain. Highest levels detected in the olfactory
 CC bulb, nucleus accumbens/olfactory tubercle, prefrontal cortex and
 CC other cortical regions, midbrain regions consisting of substantia
 CC nigra and ventral tegmentum, cerebellum, and pons/medulla. Among

peripheral tissues, highest level observed in the liver, less
 expression in kidney, gastrointestinal tract, spleen, pancreas,
 and heart.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF380186; AAK71237.1; --
 CC EMBL; AF421352; AAL65137.1; --
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSIN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Polymorphism.
 CC
 CC DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 25 45 1 (POTENTIAL).
 CC DOMAIN 46 58 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 59 79 2 (POTENTIAL).
 CC DOMAIN 80 97 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 98 118 3 (POTENTIAL).
 CC DOMAIN 119 138 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 139 159 4 (POTENTIAL).
 CC DOMAIN 160 187 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 188 208 5 (POTENTIAL).
 CC DOMAIN 209 249 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 250 270 6 (POTENTIAL).
 CC DOMAIN 271 287 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 288 308 7 (POTENTIAL).
 CC DOMAIN 309 332 CYTOPLASMIC (POTENTIAL).
 CC DISULFID 95 181 BY SIMILARITY.
 CC CARBOHYD 9 9 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC VARIANT 170 170 L -> Q.
 CC SEQUENCE 332 AA; 38021 MW; AD7F3A728C7B246 CRC64;
 Query Match 77.9%; Score 1403; DB 1; Length 332;
 Best Local Similarity 78.1%; Pred. No. 8.9e-89;
 Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;
 QY 1 MPFCHNIINISCVKNWSDVRASISYSLMWLIILITLVGNLIVIVISISHPKOLHTPTNWL 60
 Db 1 MHLCHNSANISHTNSNRDVRASISYSLISLILITLVGNLIVIVISISHPKOLHTPTNWL 60
 QY 61 IHSMATVDFLLGCLVMPYMSVRSABHCWYFGEVFCCKIHTSTDMSSASIFHLSFISIDR 120
 Db 61 LHSMAVDFLLGCLVMPYMSVRSABHCWYFGEVFCCKIHTSTDMSSASIFHLSFISIDR 120
 QY 121 YVAVCDPLRYKAKMILVICVMIFISWSVPVAFAGMIFLELNFKAEEIYKHHVHCRGG 180
 Db 121 YVAVCDPLRYKAKMILVICVMIFISWSVPVAFAGMIFLELNFKAEEIYKHHVHCRGG 180
 QY 181 CSVFPSKISGVLTFTMTSPYIPGSMILCVYRIYLIJAKQARLISDANOKLQIGLEMKNGI 240
 Db 181 CFFPSKISGVLTFTMTSPYIPGSMILCVYRIYLIJAKQARLISDANOKLQIGLEMKNGI 240
 QY 241 SOSKERKAVKTLGIYMGVFLICWCFFCTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 Db 241 SOSKERKAVKTLGIYMGVFLICWCFFCTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 QY 301 MYAFYFYPFRKALOMLFGKIFQKDSRCKLFL 334
 Db 299 MYAFYFYPFRKALOMLFGKIFQKDSRCKLFL 332

RESULT 4
TAR1 MOUSE
ID TAR1 MOUSE STANDARD; PRT; 332 AA.
AC Q923Y8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Trace amine receptor 1 (Tar-1).
GN TAR1 OR TAL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogorzalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchehek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Activated by endogenous trace amines as well as metabolites of the
CC biogenic amine neurotransmitters (By similarity). Trace amines are
CC biogenic amines present in very low levels in mammalian tissues.
CC Although some trace amines have clearly defined roles as
CC neurotransmitters in invertebrates, the extent to which they
CC function as true neurotransmitters in vertebrates has remained
CC speculative. Trace amines are likely to be involved in a variety
CC of physiological functions that have yet to be fully understood.
CC This receptor seems to be mediated by the G(s)-class of G-proteins
CC which activate adenylate cyclase (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely distributed throughout the brain.
CC Strongly expressed in the mitral cell layer of the olfactory bulb,
CC piriform cortex, the arcuate, motor, and mesencephalic trigeminal
CC nuclei, lateral reticular and hypoglossal nuclei, cerebellar
CC Purkinje cells, and ventral horn of the spinal cord. Moderately
CC expressed in the frontal, entorhinal, and agranular cortices, the
CC ventral pallidum, thalamus, hippocampus, several hypothalamic
CC nuclei, ambiguous, dorsal raphe, and gigantocellular reticular
CC nuclei. Weakly expressed in the septum, basal ganglia, amygdala,
CC myelencephalon, and spinal cord dorsal horn. Particularly
CC interesting is the moderate expression in several monoaminergic
CC cell groups, namely the dorsal raphe, the locus coeruleus, and the
CC ventral tegmental area.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF380187; AAK71238.1; -.
DR MGD; MGI:2148258; Tar1.
DR GO; GO:0016021; C:integral to membrane; IC.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR000337; GPCRHOODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 45 1 (POTENTIAL).
FT DOMAIN 46 58 CYTOPLASMIC (POTENTIAL).
FT 59 79 2 (POTENTIAL).

FT DOMAIN 80 97 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 98 118 3 (POTENTIAL).
FT DOMAIN 119 138 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 139 159 4 (POTENTIAL).
FT DOMAIN 160 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 208 5 (POTENTIAL).
FT DOMAIN 209 249 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 250 270 6 (POTENTIAL).
FT DOMAIN 271 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 7 (POTENTIAL).
FT DOMAIN 309 332 CYTOPLASMIC (POTENTIAL).
FT DISULFID 95 181 BY SIMILARITY.
FT CARBOHYD 9 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 332 AA; 37620 MW; 580BE692B1892264 CRC64;
Query Match 75.0%; Score 1351; DB 1; Length 332;
Best Local Similarity 75.4%; Pred. No. 3e-85;
Matches 252; Conservative 31; Mismatches 49; Indels 2; Gaps 1;
QY 1 MPFCHNINISCVKNNWSDVPSLYSLMVLIIILTLVGNLIVIVYISHFKQLHTPTNWL 60
Db 1 MHLCHAITNISHRNSDWSREVQASLYSLMIIILATLVGNLIVIIISISHFKQLHTPTNWL 60
QY 61 IHSMTAVDFLLGCLVMPYSWVSAHCVFGEVFCVCKIHTSTDIMLSSASIFHLSPISIDR 120
Db 61 LHSMAIVDFLLGCLVMPYSWVSAHCVFGEVFCVCKIHTSTDIMLSSASIFHLSPISIDR 120
QY 121 YVACDPLRYKAKMILVTCVMIFISWSPVAFVAFGMIFLNFKGAEEIYKHKVCRGG 180
Db 121 YVACDPLRYKAKINISTILVMILVSWSLPVAFAFGMIFLNFKGAEEIYKHKVCRGG 180
QY 181 CSVFESKISGLVTMTSTSVIPGSMICVYRYLYLAKQARLISDANOKLOIGLEWNGI 240
Db 181 CSPFFSKISGLVTMTSTSVIPGSMICVYRYLYLAKQARLISDANOKLOIGLEWNGI 240
QY 241 SOSKERKAVKTLIGVWGVFLICWCFFICTVMDPFLHIPPTLNDVLIWFGYLNSTENP 300
Db 239 PQSKETKAAKTLIGVWGVFLICWCFFICTVMDPFLHIPPTLNDVLIWFGYLNSTENP 300
QY 301 MYAFYFVWFRKALQMLFGKIFQKDSRCKLFL 334
Db 299 MYAFYFVWFRKALQMLFGKIFQKDSRCKLFL 332
RESULT 5
TAR2 RAT
ID TAR2 RAT STANDARD; PRT; 347 AA.
AC Q923Y7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Trace amine receptor 2 (Tar-2).
GN GN GN
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogorzalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchehek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Of the biogenic trace amine tested, activated only by beta-
CC phenylethylamine (beta-PEA) and tryptamine; however, the response
CC is of low potency. Trace amines are biogenic amines present in
CC very low levels in mammalian tissues. Although some trace amines

RESULT	6
GP58	HUMAN
ID_	GP58 HUMAN
STANDARD;	PRT; 306 AA.
AC	Q9P1F5;
DT	15-MAR-2004 (Rel. 43, Created)
DT	15-MAR-2004 (Rel. 43, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Probable G protein-coupled receptor GPR58.
GN	GPR58.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	
FX	MDLNAME=20149852; PubMed=106684976;

RA	Lee D.K., Lynch K.N., Nguyen L., Kim D.-S., Cheng K.T., Sankariva V.R.,
RA	Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
RA	Marchese A.;
RT	"Cloning and characterization of additional members of the G protein-
RT	coupled receptor family";
RL	Biochim. Biophys. Acta 1490:311-323 (2000) .
CC	-I- FUNCTION: Orphan receptor.
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-I- TISSUE SPECIFICITY: Not expressed in the pons, thalamus,
CC	hypothalamus, hippocampus, caudate, putamen, frontal cortex, basal
CC	forebrain, midbrain or liver.
CC	-I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

```

DR PROSITE; PSS0297; G-PROTEIN RECEPTOR FL_1; 1.
DR PROSITE; PSS0262; G-PROTEIN RECEPTOR FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 3 EXTRACELLULAR (POTENTIAL).
FT FT 4 24 TRANSMEM 1 (POTENTIAL).
FT FT 5 34 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 34 TRANSMEM 2 (POTENTIAL).
FT FT 35 55 TRANSMEM 3 (POTENTIAL).
FT DOMAIN 56 73 TRANSMEM 4 (POTENTIAL).
FT FT 74 94 TRANSMEM 5 (POTENTIAL).
FT DOMAIN 95 117 TRANSMEM 6 (POTENTIAL).
FT FT 118 138 TRANSMEM 7 (POTENTIAL).
FT DOMAIN 139 162 TRANSMEM 8 (POTENTIAL).
FT FT 163 183 TRANSMEM 9 (POTENTIAL).
FT DOMAIN 184 218 TRANSMEM 10 (POTENTIAL).
FT FT 219 239 TRANSMEM 11 (POTENTIAL).
FT DOMAIN 240 254 TRANSMEM 12 (POTENTIAL).
FT FT 255 277 TRANSMEM 13 (POTENTIAL).
FT DOMAIN 278 306 TRANSMEM 14 (POTENTIAL).
FT FT DISULFID 71 156 BY SIMILARITY.
FT CARBOHYD 244 244 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 306 AA; 34924 MW; 55629PF613062777C CRC64;

Query Match 45.3%; Score 815; DB 1; Length 306;
Best Local Similarity 50.0%; Pred. No. 7.6e-49;
Matches 158; Conservative 48; Mismatches 86; Indels 24; Gaps

```

RESULT 6

GP58_HUMAN	STANDARD;	PRT;	306 AA.
ID	Q9P1P5;		
AC	15-MAR-2004 (Rel. 43, Created)		
DT	15-MAR-2004 (Rel. 43, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Probable G protein-coupled receptor GPR58.		
GN	GPR58.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20149852; PubMed=10694976;		
RA	Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,		
RA	Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,		
RA	Marchese A.;		
RT	"cloning and characterization of additional members of the G protein-		
RL	coupled receptor family.";		
RL	Biochim. Biophys. Acta 1490:311-323 (2000).		
CC	-1- FUNCTION: Orphan receptor.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: Not expressed in the pons, thalamus,		
CC	hypothalamus, hippocampus, caudate, putamen, frontal cortex, basal		
CC	forebrain, midbrain or liver.		
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
CC	-----		
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF112460; AAP27278.1; -.		
DR	Genew; HGNC:4514; GPR58.		
DR	MTM; 604849; -.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	PFam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRHHODPSN.		
DR	PROSITE; PS00237; G PROTEIN RECEPT_F1; 1.		
DR	PROSITE; PS00262; G PROTEIN RECEPT_F2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.		
FT	DOMAIN 1 3 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 4 24 1 (POTENTIAL).		
FT	DOMAIN 25 34 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 35 55 2 (POTENTIAL).		
FT	DOMAIN 56 73 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 74 94 3 (POTENTIAL).		
FT	DOMAIN 95 117 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 118 138 4 (POTENTIAL).		
FT	DOMAIN 139 162 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 163 183 5 (POTENTIAL).		
FT	DOMAIN 184 218 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 219 239 6 (POTENTIAL).		
FT	DOMAIN 240 254 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 255 277 7 (POTENTIAL).		
FT	DOMAIN 278 306 CYTOPLASMIC (POTENTIAL).		
FT	DISULFID 71 156 BY SIMILARITY.		
FT	CARBOHYD 244 244 N-LINKED (GLCNAC...) (POTENTIAL).		
SQ	SEQUENCE 306 AA; 34924 MW; 55629PF613062777C CRC64;		

Query Match 45.3%; Score 815; DB 1; Length 306;
Best Local Similarity 50.0%; Pred. No. 7.6e-49;
Matches 158; Conservative 48; Mismatches 86; Indels 24; Gaps 4;

QY 25 LYSIMWLILITLVGNLIVIVTSISHFQKQHTPTNWLHSMATVDFLLGCLVMPYSWVRSA 84

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QY 85 EHCWTFGEVCKIHTSDIMLSASIFHLFSISIDRYAVCDPLRYKAKMNLIVCMWLP 144
Db 61 ENCWFGTGLTKIYYSFDLMLTSITSLHLCVAIDRFYALCYPLLYSTKITIPVIXKLL 120
QY 145 ISWSPVAVPARGMIFUENLNFKAEEIYYKHVHRCGCVFFKISGVLTFMTSFFYIPGSI 204
Db 121 LCWSVPGAFAFGAVFSEAYADGIEG-YDILVACSSCPVMFNKLGWTLTFMAGFFTPGSM 179
QY 205 MLCVYRYIYLLAKEQARLSD--ANQKLIQIGLEMKNGISQSKERKAVKTLGIVMGVFLIC 262
Db 180 MVIYGIKIFAVRKRKAHANN--RENNQNV-----KKDKAARTLGIIVGVFLIC 229
QY 263 WCPFFICTVMDPFLHVIIPPTLNDVLIWFGYLNSTENPMVYAFFYFWRKAKMMLFGKI 322
Db 230 WPCPFTILLDFLNESTPVLFDALTWFGYFNSTCNPLIYGFYFWRFRALKYIILGKI 289
QY 323 P-----QKDS 327
Db 290 FSSCFHNTILCMQKES 305

RESULT 7
GP57_HUMAN
ID GP57_HUMAN STANDARD; PRT; 343 AA.
AC Q9P1P4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable G protein-coupled receptor GPR57.
GN GPR57.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149852; PubMed=10684976;
RA Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,
RA Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
RA Marchese A.;
RT Cloning and characterization of additional members of the G protein-
RT coupled receptor family."
RL Biochim. Biophys. Acta 1490:311-323 (2000).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Not expressed in the pons, thalamus, globus
CC pallidus, caudate, putamen or cerebellum.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF112461; AAF27279.1; -.
CC Genbank; HGNC:4513; GPR57.
CC MIM; 604848; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 56 1 (POTENTIAL).
FT DOMAIN 57 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 150 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 151 168 3 (POTENTIAL).
FT DOMAIN 169 172 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 173 193 4 (POTENTIAL).
FT DOMAIN 194 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 223 5 (POTENTIAL).
FT DOMAIN 224 257 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 258 278 6 (POTENTIAL).
FT DOMAIN 279 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 7 (POTENTIAL).
FT DOMAIN 309 343 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 343 AA; 39065 MW; DC513D15ABBC026F CRC64;

Query Match 45.2%; Score 813.5; DB 1; Length 343;
Best Local Similarity 46.0%; Pred. No. 1.1e-48;
Matches 159; Conservative 57; Mismatches 99; Indels 31; Gaps 5;

QY 4 CHNIN-----ISCVKNN-----WSNDVRASLYSLMVLIIITLTVGNLIIVVISI 49
Db 13 CPKFNKILSSHQPLFSCPGDNVFGYDWSHDY-----PLFGNLIVMVISI 58
QY 50 FKQLHTPTNMLIHSMTATVDFLLGCLVMPYSMSVRSAEHCWYFGEVFCCKIHTSDIMLSAS 109
Db 59 FKQLHSPTNFLILSMATTDLLGLGVIMPYSIMRSVESCWYFGDGCKFTSDDMLRLTS 118
QY 110 IFHLSPISIDRYAVCDPLRYKAKMNLIVCMIFISWSPVAVFAFGMIFLELNFKGAE 169
Db 119 IFHLCSIAIDRFYAVCYPLHYTKNTSTIKOLLAFCSVPALFSGVLSEADVSGMQS 178
QY 170 IYKHVHRCGCVFFKISGVLTFMTSPYIPGSMVCVYIYLIKQARLISDANQK 229
Db 179 -YKILVACFNFCALTFFNKFWGTILFTTCFFTPGSMVGIYKIFIVSKQHARVISHPEN 237
QY 230 LQIGLEMKNGISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHVIIPPTLNDVLI 289
Db 238 TKGA--VKHLSKKDKRAAKTLGIVMGVFLACWLPCLFVLAVLDPLDLYSTLILDLIV 295
QY 290 WFGYLNSTENPMVYAFFYFWRKAKMMLFGKIFQKDSRCKLFL 335
Db 296 WLRYFNSTCNPLIHGFFNFWQKAFKIVSGKIFSSHSETANLFE 341

RESULT 8
TAR3_RAT
ID TAR3_RAT STANDARD; PRT; 338 AA.
AC Q923Y6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Trace amine receptor 3 (Tar-3).
GN TAR3 OR TA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971 (2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Trace amines are biogenic amines present in very low levels in
CC mammalian tissues. Although some trace amines have clearly defined
CC roles as neurotransmitters in invertebrates, the extent to which
CC they function as true neurotransmitters in vertebrates has
CC remained speculative. Trace amines are likely to be involved in a
CC variety of physiological functions that have yet to be fully
CC understood.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

```

CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sib.ch/commerce/
CC	or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL: AF380190; AAK71241.1; ..
DR	InterPro: IPR000276; GPCR_Rhodpsn.
DR	Pfam: PF00001; 7tm.1; 1.
DR	PRINTS; PR00237; GPCRHHODPSN.
DR	PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR	PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Multigene family.
FT	DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 24 44 1 (POTENTIAL).
FT	DOMAIN 45 58 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 59 79 2 (POTENTIAL).
FT	DOMAIN 80 97 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 98 118 3 (POTENTIAL).
FT	DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 138 158 4 (POTENTIAL).
FT	DOMAIN 159 187 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 188 208 5 (POTENTIAL).
FT	DOMAIN 209 249 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 250 270 6 (POTENTIAL).
FT	DOMAIN 271 284 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 285 305 7 (POTENTIAL).
FT	DOMAIN 306 338 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 95 180 BY SIMILARITY.
FT	CARBOHYD 3 9 N-GLYCOSYL (GLCNAC..) (POTENTIAL).
CC	SEQUENCE 338 AA; 37846 MW; F8BC058A21664EA4 CRC64;
CC	-----

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Query Match          43.4%; Score 782; DB 1; Length 338;
Best Local Similarity 45.8%; Pred. No. 1.4e-46;
Matches 154; Conservative 63; Mismatches 115; Indels 4; Gaps 4;

QY 1 MPFCHNLIINISCVQNNNSNDVRASLYSIWLVIILITLVGNLIVISISHPKQLHTPTNWL 60
DB 1 MELCYENVNGSCIKSSSPRPRLAYVGLGALLAVFNLVITALHFKQLHTPTNFL 60
QY 61 IHSMATYDFLLGCLVMPYSVRSAEHCWYGEVECKIHTTDMILMSASIFHLFSIDR 120
DB 61 VASLACADFLVGVTMPFSTVRSVEGCWYFGDTYCKFTCFDTSFCFASLFLHLCISIDR 120
QY 121 YYAVCDPLRYKAKNNILVICMIIFISNSVPAVFAFGMIFLELNFKGAEIYYKHVHCRRG 180
DB 121 YVAVTDPLTPTKRTIISVSGVCIALSFFVSYSFSFYTGANEEGEELVVA-LTVCVG 179
QY 181 CSVPFISGISVLTPEMTSTFYIPGSIIMLCVYIRYILIAKEQARLI-SDANQKIQIGLEMKG 239
DB 180 CQAPLNQNNWLLCFLL-FFLPTVVMVFLYGRIFLVAQQARKIBGSANQPAASSESYKER 238
QY 240 ISOSKERKAVKTLGIVMGVFLIICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVLNTFN 299
DB 239 VAR-RERKAAKTLGIAAAFLVSLPFIIDAVIDVMFNFTPAYVYBILVMCVVYNSAMN 297
QY 300 PMVYARFYPWFRKALKWMLFGKIFQKDSRCKKFLF 335
DB 298 PLIIAFYPWFRKALKIIVSGKVFRASSRTNLFSE 333

RESULT 9
TAR3 HUMAN
ID -TAR3 HUMAN STANDARD; PRT; 348 AA.
AC Q96R19;
DT 15-MAR-2004 (Rel. 43, Created)
DD 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

```

Trace amine receptor 3 (TaR-3).

TAR3 OR TAR3.

Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

MEDLINE=21374364; PubMed=11459929;

Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R., Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S., Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y., Branchette T.A., Gerald C.;

"Trace amines: Identification of a family of mammalian G protein-coupled receptors.";

Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).

[2]

SEQUENCE FROM N.A.

Kopatz S.A., Aronstam R.S., Sharma S.V.;

"CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.

Trace amines are biogenic amines present in very low levels in mammalian tissues. Although some trace amines have clearly defined roles as neurotransmitters in invertebrates, the extent to which they function as true neurotransmitters in vertebrates has remained speculative. Trace amines are likely to be involved in a variety of physiological functions that have yet to be fully understood.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF380189; AA071240.1; -

EMBL; AY183469; AA024660.1; -

InterPro; IPR000276; GPCR_Rhodopsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHHODOPS.

PROSITE; PS00237; G PROTEIN RECP FL 1; 1.

PROSITE; PS0262; G-PROTEIN-RECP-FL-2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.

DOMAIN	1	37	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	38	1 (POTENTIAL).
FT	DOMAIN	59	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	69	2 (POTENTIAL).
FT	DOMAIN	90	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	107	3 (POTENTIAL).
FT	DOMAIN	129	147
FT	TRANSMEM	148	168
FT	DOMAIN	169	197
FT	TRANSMEM	198	218
FT	DOMAIN	219	259
FT	TRANSMEM	260	280
FT	DOMAIN	281	294
FT	TRANSMEM	295	315
FT	DOMAIN	316	348
FT	DISULFID	105	190
FT	CARBOHYD	4	4
FT	CARBOHYD	19	19
SEQUENCE	348 AA;	39016 MW;	D0C6484880A6F761 CRC64;

Query Match 41.3%; Score 743; DB 1; Length 348;

Best Local Similarity 42.5%; Pred. No. 6.6e-44;

Matches 141; Conservative 63; Mismatches 126; Indels 2; Gaps 2;

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QY 4 CHNIINISCVKNWNSDVASLSYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWLHS 63
DB 14 CYKNVNESCKTPYSGPRSSIIYAVLGFAGVAAAGNLLMVAIIHLFKQLHTPTNPLIAS 73
QY 64 MATVDLFLGCLVMPYSMSVRSABHCVYGFVKIHTSTDIMLSSASIFHLSPISIDRYVA 123
DB 74 LACADFVLGVTPWPFSTVRSVSVSGYSGYKFKHTCFDTSFCFASLFLHLCISVDRYTA 133
QY 124 VCDPLRYKAKMNLIVICWMIFISWSVPAVAFGMIFLEINFGABEIIYKHVHCRCGCV 183
DB 134 VTDPLTYPTKFTVSVSGICIVLSWFFSVTYSFIYTGANEGIEBELVVA-LTCVGGCOA 192
QY 184 PFSKISGVLTFMTSVFIPGSMILCVYRIYLAKQARLISDANKQLQIGLEMKNGISQS 243
DB 193 PLNQWVLLCFLL-FEIPNVAVFYISKIFLVAQKQAKIESTASQSSSSYKERVAK 251
QY 244 KERKAVKTIGIYMGVFLICWCPCFFICTVMDPPLHYIIPPLNDVLIVFGYLNSTENPMVY 303
DB 252 RERKAATLGIAMAAFLVSWLPYLDVDAVIDAYMNFITPPYVVEILVWCYVYNSAMNPLIY 311
QY 304 AFYFYPWFRKALKMMLFGKIFQKDSRCKLFLE 335
DB 312 AFYQWFGKAIKLIYSGKVLRTDSTTNLFSE 343
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RESULT 10
TAR12 RAT
ID TAR12 RAT STANDARD; PRT; 333 AA.
AC Q923X8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Trace amine receptor 12 (Tar-12).
GN TAR12 OR TAR12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.;
RA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971 (2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Trace amines are biogenic amines present in very low levels in
CC mammalian tissues. Although some trace amines have clearly defined
CC roles as neurotransmitters in invertebrates, the extent to which
CC they function as true neurotransmitters in vertebrates has
CC remained speculative. Trace amines are likely to be involved in a
CC variety of physiological functions that have yet to be fully
CC understood.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF380200; AAK71251.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
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DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 23 43 1 (POTENTIAL).
FT DOMAIN 44 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 79 2 (POTENTIAL).
FT DOMAIN 80 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 118 3 (POTENTIAL).
FT DOMAIN 119 141 4 (POTENTIAL).
FT TRANSMEM 142 162 4 (POTENTIAL).
FT DOMAIN 163 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 207 5 (POTENTIAL).
FT TRANSMEM 208 249 6 (POTENTIAL).
FT DOMAIN 250 270 6 (POTENTIAL).
FT TRANSMEM 271 283 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 284 305 7 (POTENTIAL).
FT TRANSMEM 306 333 7 (POTENTIAL).
FT DOMAIN 334 353 7 (POTENTIAL).
FT DISULFID 95 180 BY SIMILARITY.
FT CARBOHYD 9 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 333 AA; 37467 MW; 65BD886131C1C85B CRC64;
Query Match 41.1%; Score 741; DB 1; Length 333;
Best Local Similarity 41.8%; Pred. No. 8.7e-44;
Matches 140; Conservative 70; Mismatches 123; Indels 2; Gaps 2;
QY 1 MPFCNINISCVKNWNSDVASLSYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 60
DB 1 MOLCEKLNRCVSPYSGPRLLIYAVFGFAGVAAAGNLLMVAIIHLFKQLHTPTNPL 60
QY 61 IHSMTATVDLGLVMPYSMSVRSABHCVYGFVKIHTSTDIMLSSASIFHLSPISIDR 120
DB 61 VASLACADFVLGVTPWPFSTVRSVSVSGYSGYKFKHTCFDTSFCFASLFLHLCIS 120
QY 121 YVAVCDPLRYKAKMNLIVICWMIFISWSVPAVAFGMIFLEINFGABEIIYKHVHC 180
DB 121 YVAVSDPLIYPRFTASVSGKCIITFSWLLSIYVSFLVGTWNEAGLEDL-VSALT 179
QY 181 CSVFSKISGVLTFMTSVFIPGSMILCVYRIYLAKQARLISDANKQLQIGLEMKNGI 240
DB 180 COIYVNSQWVFINFLL-FLVPALVMTVYISKIFLAKQAOQNIERKMGKTARASEY 238
QY 241 SQSKERKAVKTIGIYMGVFLICWCPCFFICTVMDPPLHYIIPPLNDVLIVFGYLN 300
DB 239 VAKRERKAATLGIAMAAFLVSWLPYLDVDAVIDAYMNFITPPYVVEILVWCYV 298
QY 301 MYAFYFYPWFRKALKMMLFGKIFQKDSRCKLFLE 335
DB 299 LIYAFYFYPWFRKAIKLIYSGKILRENSATNLFPE 333
RESULT 11
TAR7 RAT
ID TAR7 RAT STANDARD; PRT; 344 AA.
AC Q923Y3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Trace amine receptor 7 (Tar-7).
GN TAR7 OR TAR7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.;
RA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971 (2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Trace amines are biogenic amines present in very low levels in
CC mammalian tissues. Although some trace amines have clearly defined
CC roles as neurotransmitters in invertebrates, the extent to which
CC they function as true neurotransmitters in vertebrates has
CC remained speculative. Trace amines are likely to be involved in a
CC variety of physiological functions that have yet to be fully
CC understood.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF380200; AAK71251.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
```



```
"Trace amines: Identification of a family of mammalian G protein-  
coupled receptors";  
Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).  
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mammalian tissues. Although some trace amines have clearly defined  
roles as neurotransmitters invertebrates, the extent to which  
they function as true neurotransmitters in vertebrates has  
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CC SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
  
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or send an email to license@isb-sib.ch)  
  
EMBL; AF380195; AAK71246.1; -.  
DR InterPro: IPR000276; GPCR_Rhodpsn.  
DR Pfam: PFOO001; 7cm_1; 1.  
DR PRINTS; PR00237; GCRRHODOPSN.  
DR PROSITE; PS00237; G PROTEIN RECEPT F1 1; 1.  
DR PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Multigene family.  
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 34 54 1 (POTENTIAL).  
FT DOMAIN 55 67 CYTOPLASMIC (POTENTIAL).  
FT TRANSME 68 88 2 (POTENTIAL).  
FT DOMAIN 89 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 103 127 3 (POTENTIAL).  
FT DOMAIN 128 146 4 (POTENTIAL).  
FT TRANSME 147 167 5 (POTENTIAL).  
FT DOMAIN 168 196 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 197 217 5 (POTENTIAL).  
FT DOMAIN 218 256 CYTOPLASMIC (POTENTIAL).  
FT TRANSEM 257 277 6 (POTENTIAL).  
FT DOMAIN 278 295 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 296 319 7 (POTENTIAL).  
FT DOMAIN 320 344 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 104 189 BY SIMILARITY.  
FT CARBOHYD 4 4 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 18 18 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 344 AA; 38043 MW; 45C41C86IESF6408 CRC64;
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Query Match 40.7%; Score 733; DB 1; Length 344;
Best Local Similarity 41.2%; Pred. No. 3 le-43;
Matches 139; Conservative 73; Mismatches 121; Indels 4; Gaps 3;

QY		1	MPCNHNIISCVKNNSNDVRASLSMLVLIILTTLVGNLIVIVISHFKQLHTPTNW L	60
Dd		10	LQLCYENVNASCIKTPYPGRLRVLLVMVFQGAVLAFCGNLLVVSVLFHFQKLHS PANFL	69
Qy		61	IHSWATVDLLGLGVMPYSMVRAEHCWFGEVPCKIHSTDTIMLSASIHFHSPTS IDR	120
Dd		70	IASLASADFVLIGVSIMPFPMSVRGISWCWFGDFTCSLSHSCDDAAFCYSSLFHL CFI SVDR	129
Qy		121	VYAACPDLRYKAAMNILVICMIFIFSWSVAFAFMGFLELNFKGAEEIYYKHVCRCG	180
Dd		130	VIATEPLYPTFTWSVSGICISISWLPLTVSSAVFYTGISTGIENLV-SALNCVGG	188
Qy		181	CSVFFSKISGVLTMTSFYIPGSIMLCVYYRIYLIAKEQA RL--SDANQKIQIGLEM KN	238
Dd		189	CQAINQDWLISFL--FRPIITLMIIYSKFELVAKQAVKIETSI SGKSSESSL SHK	247
Qy		239	GISOEKERKAVKITLGVMGVFLCWCPFFTCTVTMDPFPHVIPPTLDNVLI WPGYN STF	298
Dd		248	ARKXBERKA AKT LGVTWMAFVSWLPYTITDILD FMGFI TPAYVVEYCWTAY NSAM	307


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RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RA MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Trace amines are biogenic amines present in very low levels in
CC mammalian tissues. Although some trace amines have clearly defined
CC roles as neurotransmitters in invertebrates, the extent to which
CC they function as true neurotransmitters in vertebrates has
CC remained speculative. Trace amines are likely to be involved in a
CC variety of physiological functions that have yet to be fully
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CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC -----
CC EMBL; AF380198; AAK71249.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family.
CC DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 37 57 1 (POTENTIAL).
CC DOMAIN 58 67 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 68 88 2 (POTENTIAL).
CC DOMAIN 89 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 127 3 (POTENTIAL).
CC DOMAIN 128 146 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 147 167 4 (POTENTIAL).
CC DOMAIN 168 196 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 197 217 5 (POTENTIAL).
CC DOMAIN 218 260 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 261 281 6 (POTENTIAL).
CC DOMAIN 282 295 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 296 319 7 (POTENTIAL).
CC DOMAIN 320 344 CYTOPLASMIC (POTENTIAL).
CC DISULFID 96 189 BY SIMILARITY.
CC CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 18 18 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 344 AA; 38015 MW; 6AB7A50CE3BEB92 CRC64;

Query Match 40.5%; Score 730; DB 1; Length 344;
Best Local Similarity 41.2%; Pred. No. Se-43;
Matches 139; Conservative 71; Mismatches 123; Indels 4; Gaps 3;

QY 1 MPFCHNINISCVKKNWSDVRSYLSVLMLVLLITLVNGLVIVISISHFKOLHTPTWNL 60
DB 10 LQLCENVNASCKITPTSPGLVLLYVMVFGGAVLAVCGNLLVLSVLHFKOLHSPANFL 69
QY 61 IHSMATVDPLGLCLVMPYSWRSABHCWYFGVFCIKHTSTDMLSASIFHLSISIDR 120
DB 70 IASLASADFLVGSVMPFSWRSIESCWYFGTFCSLHSCCDVAFCYSSALHLCISVDR 129
QY 121 YVAVCDPLRYKAMMLVLCVMIFTSVSWPVAFVAFGMIFLENFKGAEIYYKHVCRGG 180
DB 130 VIAVTDPLVYPTKFTVSVSGICISISWILPLVYSSAVFVTGTSAMGIENL-VSALNCVGG 188

QY 181 CSVFESKISGVLTMTSTFVIPGIMLCVYRIVYIATAEQARLI--SDANQKLOIGLEMKN 238
DB 189 CQVVVNQDWLISFL--FFIPTVMIILYSKIFLVAQOAVKIETSVSGSKGESSLESHK 247
QY 239 GISQSKERKAVKTLGIVMGVFLICWPPFCIFWMDPPFLHILIPPTLNDVLINFGYLNSTF 298
DB 248 ARVAKRERKAAKTLGTVLAFIVSWLPYITDILDAFMGFTIPAYVVEFCSSAYNSAM 307
QY 299 NPMVTAFYPFPRKALKMMLFKQIFQKSSRCKLFLE 335
DB 308 NPLIYAFYFPRKAMKILSGKILKGHSSTTSLESE 344

RESULT 15
TAL4 RAT
ID TAL4 RAT STANDARD; PRT; 358 AA.
AC Q923X6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Trace amine receptor 14 (Tar-14).
GN TAR14 OR TAL4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
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RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Trace amines are biogenic amines present in very low levels in
CC mammalian tissues. Although some trace amines have clearly defined
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CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC
CC -----
CC EMBL; AF380198; AAK71249.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family.
CC DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 37 57 1 (POTENTIAL).
CC DOMAIN 58 67 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 68 88 2 (POTENTIAL).
CC DOMAIN 89 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 127 3 (POTENTIAL).
CC DOMAIN 128 146 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 147 167 4 (POTENTIAL).
CC DOMAIN 168 196 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 197 217 5 (POTENTIAL).
CC DOMAIN 218 260 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 261 281 6 (POTENTIAL).
CC DOMAIN 282 295 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 296 319 7 (POTENTIAL).
CC DOMAIN 320 344 CYTOPLASMIC (POTENTIAL).
CC DISULFID 96 189 BY SIMILARITY.
CC CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 18 18 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 344 AA; 38015 MW; 6AB7A50CE3BEB92 CRC64;

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GenCore version 5.1.6
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 OM protein - protein search, using sw model
 Run on: October 8, 2004, 10:16:35 ; Search time 44 Seconds
 (without alignments)
 2423.753 Million cell updates/sec

Title: US-09-633-145-2
 Perfect score: 1801
 Sequence: 1 MPFCHNIINISCKVNSND.....FGKIFQDSSRCKLFLSLSS 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	1801	100.0	339	4	Q96RJ0		Q96rj0 homo sapien
2	1757	97.6	338	6	Q8HZ64		Q8hz64 macaca mulla
3	1403	77.9	332	11	Q923Y9		Q923y9 rattus norv
4	1398	77.6	332	11	Q8VH05		Q8vhq5 rattus norv
5	1351	75.0	332	11	Q923Y8		Q923y8 mus musculu
6	927.5	51.5	347	11	Q923Y7		Q923y7 rattus norv
7	815	45.3	306	4	Q9P1P5		Q9p1p5 homo sapien
8	813.5	45.2	343	4	Q9P1P4		Q9p1p4 homo sapien
9	782	43.4	338	11	Q923Y6		Q923y6 rattus norv
10	743	41.3	348	4	Q96R19		Q96r19 homo sapien
11	741	41.1	333	11	Q923X8		Q923x8 rattus norv
12	733	40.7	344	11	Q923Y3		Q923y3 rattus norv
13	732	40.6	345	11	Q923Y5		Q923y5 rattus norv
14	731	40.6	374	11	Q923X9		Q923x9 rattus norv
15	730	40.5	344	11	Q923Y0		Q923y0 rattus norv
16	722	40.1	358	11	Q923X6		Q923x6 rattus norv

17	722	40.1	358	11	Q923X5	Q923x5 rattus norv
18	715	39.7	345	4	Q96R18	Q96r18 homo sapien
19	713	39.6	358	11	Q923Y2	Q923y2 rattus norv
20	710	39.4	358	11	Q923Y1	Q923y1 rattus norv
21	704	39.1	358	11	Q923Y4	Q923y4 rattus norv
22	679	37.7	362	11	Q923X7	Q923x7 rattus norv
23	677.5	37.6	337	4	O14804	O14804 homo sapien
24	580.5	32.2	352	13	Q9YHY4	Q9yhy4 lampetra fl
25	545.5	30.3	328	13	Q9YHV8	Q9yvh8 figu rubrip
26	534	29.7	387	4	Q96K10	Q96k10 homo sapien
27	534	29.7	388	4	Q8IXH9	Q8ixh9 homo sapien
28	526.5	29.2	328	13	Q9YHV7	Q9yvh7 figu rubrip
29	511	28.4	353	13	Q9YHY3	Q9yhy3 lampetra fl
30	503	27.9	446	13	O42315	O42315 cyprinus ca
31	498.5	27.7	445	13	Q98842	Q98842 anguilla an
32	495	27.5	437	13	O42316	O42316 cyprinus ca
33	488.5	27.1	358	11	Q9QX37	Q9qx37 mus musculu
34	488.5	27.1	397	11	Q9D282	Q9d282 mus musculu
35	488.5	27.1	445	13	Q98841	Q98841 anguilla an
36	481	26.7	448	13	Q98844	Q98844 anguilla an
37	477	26.5	508	5	Q9VCZ3	Q9vcz3 drosophila
38	476.5	26.5	458	13	Q98843	Q98843 anguilla an
39	473	26.3	374	11	Q8BUW7	Q8buw7 mus musculu
40	472.5	26.2	391	5	O96716	O96716 branchiosto
41	472.5	26.2	397	4	O725R9	O725r9 homo sapien
42	464	25.8	446	6	Q8WND7	Q8wnd7 bos taurus
43	462	25.7	394	5	Q9NHF3	Q9nhf3 aplysia cal
44	461	25.6	394	5	Q9NJS6	Q9njs6 aplysia kur
45	459	25.5	377	6	Q9N263	Q9n263 sus scrofa

ALIGNMENTS

RESULT 1

Q96RJ0 PRELIMINARY; PRT; 339 AA.
 AC Q96RJ0;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Trace amine receptor 1 (Putative catecholamine receptor).
 GN TAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21374364; PubMed=11459929;
 RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
 RA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
 RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
 RA Brancheck T.A., Gerald C.;
 RA "Trace amines: Identification of a family of mammalian G protein-
 coupled receptors.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21580235; PubMed=11723224;
 RA Bunzow J.R., Sonders M.S., Arttamangkul S., Harrison L.M., Zhang G.,
 RA Quigley D.I., Darland T., Suchland K.L., Pasumamula S., Kennedy J.L.,
 RA Olson S.B., Magenis R.E., Amara S.G., Grandy D.K.;
 RA "Amphetamine, 3,4-methylenedioxymethamphetamine, lysergic acid
 diethylamide, and metabolites of the catecholamine neurotransmitters
 are agonists of a rat trace amine receptor.";
 RL Mol. Pharmacol. 60:1181-1188(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RA "Isolation of cDNA coding for Human Trace Amine Receptor (TAR)1.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

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CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380185; AAK71236.1; -.
DR EMBL; AF200627; AAG17112.1; -.
DR EMBL; AY180374; AAO22154.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 339 AA; 39091 MW; 5E72FA61CEFA0E0 CRC64;

Query Match 100.0%; Score 1801; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.4e-159;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSDVRSIYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNWNSDVRSIYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 THSMATVDFLLGCLVMPYSWRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 62 THSMATVDFLLGCLVMPYSWRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFKGABEIIYKHHVCRGG 180
DB 122 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFKGABEIIYKHHVCRGG 181
QY 181 CSVFESKISGVLTFTSFYIPGIMLCVYRIYLIYLAKEQARLISDANQKLIQGLEMKNGI 240
DB 182 CSVFESKISGVLTFTSFYIPGIMLCVYRIYLIYLAKEQARLISDANQKLIQGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
QY 301 MYAIFYFWFRKALKNMFLGKIFQKDSRCKLFLELSS 338
DB 302 MYAIFYFWFRKALKNMFLGKIFQKDSRCKLFLELSS 339

RESULT 2
QBHZ64
ID Q8HZ64 PRELIMINARY; PRT; 338 AA.
AC Q8HZ64;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Trace amine receptor 1.
GN TARI.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Miller G.M., Madras B.K.;
RT "Cloning of Trace Amine Receptor 1 (TAR1) from Rhesus Monkey.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY135366; AAN06172.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.

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DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW Receptor.
SQ SEQUENCE 338 AA; 38797 MW; 9EE7B35456BB409B CRC64;

Query Match 97.6%; Score 1757; DB 6; Length 338;
Best Local Similarity 96.4%; Pred. No. 2.9e-155;
Matches 326; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSDVRSIYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 60
DB 1 MPFCHNIINISCVKNWNSDVRSIYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 60
QY 61 THSMATVDFLLGCLVMPYSWRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 61 THSMATVDFLLGCLVMPYSWRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFKGABEIIYKHHVCRGG 180
DB 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFKGABEIIYKHHVCRGG 180
QY 181 CSVFESKISGVLTFTSFYIPGIMLCVYRIYLIYLAKEQARLISDANQKLIQGLEMKNGI 240
DB 181 CSVFESKISGVLTFTSFYIPGIMLCVYRIYLIYLAKEQARLISDANQKLIQGLEMKNGI 240
QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
QY 301 MYAIFYFWFRKALKNMFLGKIFQKDSRCKLFLELSS 338
DB 301 MYAIFYFWFRKALKNMFLGKIFQKDSRCKLFLELSS 338

RESULT 3
Q923Y9
ID Q923Y9 PRELIMINARY; PRT; 332 AA.
AC Q923Y9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Trace amine receptor 1.
GN TARI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380186; AAK71237.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 332 AA; 38021 MW; ADF3A728C77B246 CRC64;

Query Match 77.9%; Score 1403; DB 11; Length 332;

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Best Local Similarity 78.1%; Pred. No. 2.5e-122; Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;	
QY 1	MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKLTPTNWL 60
Db 1	MHLCHNSANISHTNSNWRDVRASLYSLIILITLVGNLIVIVISHFQKLTPTNWL 60
QY 61	IHSMATVDLLGLVMPYSWVRSABHCWYFGEVCKHTSTDMLSASIFHLSPFISIDR 120
Db 61	LHSMATVDLLGLVMPYSWVRSABHCWYFGEVCKHTSTDMLSASIFHLSPFISIDR 120
QY 121	YAVCDPLRYKAKNNILVICVMFISWSPVAFAGMIFLELNFKGAEEIYKHKVCRGG 180
Db 121	YAVCDPLRYKAKNNILVICVMFISWSPVAFAGMIFLELNFKGAEEIYKHKVCRGG 180
QY 181	CSVFESKISGVLTFMTSFYIPGSMICVYRYIYIAKEQARLISDANQKIQIGLEMKNGI 240
Db 181	CSVFESKISGVLTFMTSFYIPGSMICVYRYIYIAKEQARLISDANQKIQIGLEMKNGI 240
QY 241	SOSKERKAVKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVNSTENP 300
Db 241	SOSKERKAVKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVNSTENP 300
QY 239	POSKETKAAKTIGIMVGVELLCWCPFFFCWLDPLGYVIPPPTLNDLWFGYLSAFNP 298
Db 239	POSKETKAAKTIGIMVGVELLCWCPFFFCWLDPLGYVIPPPTLNDLWFGYLSAFNP 298
QY 301	MYAFYFPWFRKALKMVLFGKIFQKDSRSKFL 334
Db 301	MYAFYFPWFRKALKMVLFGKIFQKDSRSKFL 334
RESULT 4	
QY Q8VHQ5	PRELIMINARY; PRT; 332 AA.
AC Q8VHQ5	PRELIMINARY; PRT; 332 AA.
DT 01-MAR-2002 (TremBLrel. 20, Created)	
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)	
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)	
DE Trace amine receptor 1.	
OS Rattus norvegicus (Rat).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	
OX NCBI_TaxID=10116;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=Sprague-Dawley;	
RX MEDLINE=21580235; PubMed=11723224;	
RA Bunzow J.R., Sonders M.S., Arttamangkul S., Harrison L.M., Zhang G.,	
RA Quigley D.I., Darland T., Suchland K.L., Pasumamula S., Kennedy J.L.,	
RA Olson S.B., Megenis E., Amara S.G., Grandy D.K.;	
RT "Amphetamine, 3,4-methylenedioxymethamphetamine, lysergic acid	
RT diethylamide, and metabolites of the catecholamine neurotransmitters	
RT are agonists of a rat trace amine receptor.";	
RL Mol. Pharmacol. 60:1181-1188(2001).	
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR EMBL; AF421352; AAL65137.1; -.	
DR GO; GO:0016021; C:integral to membrane; IEA.	
DR GO; GO:0004872; F:receptor activity; IEA.	
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.	
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.	
DR InterPro; IPR000276; GPCR_Rhodpsn.	
DR Pfam; PF00001; 7tm1.1; 1.	
DR PRINTS; PR00237; GPCRHHODOPSN.	
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.	
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.	
KW G-protein coupled receptor; Receptor; Transmembrane.	
SQ SEQUENCE 332 AA; 38036 MW; B6F519AFBADA0ECB6 CRC64;	
Query Match	
Best Local Similarity 77.6%; Score 1398; DB 11; Length 332;	
Matches 261; Conservative 26; Mismatches 45; Indels 2; Gaps 1;	
QY 1	MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKLTPTNWL 60
Db 1	MHLCHNSANISHTNSNWRDVRASLYSLIILITLVGNLIVIVISHFQKLTPTNWL 60
Best Local Similarity 78.1%; Pred. No. 7.3e-122; Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;	
QY 1	MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKLTPTNWL 60
Db 1	MHLCHNSANISHTNSNWRDVRASLYSLIILITLVGNLIVIVISHFQKLTPTNWL 60
QY 61	IHSMATVDLLGLVMPYSWVRSABHCWYFGEVCKHTSTDMLSASIFHLSPFISIDR 120
Db 61	LHSMATVDLLGLVMPYSWVRSABHCWYFGEVCKHTSTDMLSASIFHLSPFISIDR 120
QY 121	YAVCDPLRYKAKNNILVICVMFISWSPVAFAGMIFLELNFKGAEEIYKHKVCRGG 180
Db 121	YAVCDPLRYKAKNNILVICVMFISWSPVAFAGMIFLELNFKGAEEIYKHKVCRGG 180
QY 181	CSVFESKISGVLTFMTSFYIPGSMICVYRYIYIAKEQARLISDANQKIQIGLEMKNGI 240
Db 181	CSVFESKISGVLTFMTSFYIPGSMICVYRYIYIAKEQARLISDANQKIQIGLEMKNGI 240
QY 241	SOSKERKAVKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVNSTENP 300
Db 241	SOSKERKAVKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVNSTENP 300
QY 239	POSKETKAAKTIGIMVGVELLCWCPFFFCWLDPLGYVIPPPTLNDLWFGYLSAFNP 298
Db 239	POSKETKAAKTIGIMVGVELLCWCPFFFCWLDPLGYVIPPPTLNDLWFGYLSAFNP 298
QY 301	MYAFYFPWFRKALKMVLFGKIFQKDSRSKFL 334
Db 301	MYAFYFPWFRKALKMVLFGKIFQKDSRSKFL 334
RESULT 5	
QY Q923Y8	PRELIMINARY; PRT; 332 AA.
AC Q923Y8	PRELIMINARY; PRT; 332 AA.
DT 01-DEC-2001 (TremBLrel. 19, Created)	
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)	
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)	
DE Trace amine receptor 1.	
GN TAR1 OR TAR1.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX NCBI_TaxID=10090;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=129/SvJ;	
RX MEDLINE=21374364; PubMed=11459929;	
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,	
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,	
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,	
RA Branchek T.A., Gerald C.;	
RT "Trace amines: Identification of a family of mammalian G protein-	
RT coupled receptors.";	
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).	
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR EMBL; AF380187; AAK71238.1; -.	
DR MGD; MGI:2148258; Tar1.	
DR GO; GO:0016021; C:integral to membrane; IC.	
DR InterPro; IPR000276; GPCR_Rhodpsn.	
DR Pfam; PF00001; 7tm1.1; 1.	
DR PRINTS; PR00237; GPCRHHODOPSN.	
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.	
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.	
KW G-protein coupled receptor; Receptor; Transmembrane.	
SQ SEQUENCE 332 AA; 37620 MW; 680BE692B1892264 CRC64;	
Query Match	
Best Local Similarity 75.0%; Score 1351; DB 11; Length 332;	
Matches 252; Conservative 31; Mismatches 49; Indels 2; Gaps 1;	
QY 1	MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKLTPTNWL 60
Db 1	MHLCHAIINISHRNSDWSREVSASLYSLMIIILATLVGNLIVIVISHFQKLTPTNWL 60
QY 61	IHSMATVDLLGLVMPYSWVRSABHCWYFGEVCKHTSTDMLSASIFHLSPFISIDR 120
Db 61	LHSMATVDLLGLVMPYSWVRSABHCWYFGEVCKHTSTDMLSASIFHLSPFISIDR 120
QY 121	YAVCDPLRYKAKNNILVICVMFISWSPVAFAGMIFLELNFKGAEEIYKHKVCRGG 180
Db 121	YAVCDPLRYKAKNNILVICVMFISWSPVAFAGMIFLELNFKGAEEIYKHKVCRGG 180

Db 121 YCAVCDPLRYKAKINISTILVWLSVSLPAVYAFQGMIFLELNKGVBEIYRSQVSDLGG 180
 Qy 181 CSVFESKISGLVTEMTSPYIPQSIMLCVYRYIYLIAKEQARLISDANKLQIGLEMKNGI 240
 Db 181 CSVFESKISGLVTEMTSPYIPQSIMLCVYRYIYLIAKEQARLISDANKLQIGLEMKNGI 240
 Qy 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 300
 Db 239 PQSKETKAATLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 298
 Qy 301 MYAFYFVWFRKALKMFLGKIFQKDSRSRCKLFL 334
 Db 299 MYAFYFVWFRKALKMFLGKIFQKDSRSRCKLFL 332

RESULT 6

Q923Y7 ID Q923Y7 PRELIMINARY; PRT; 347 AA.
 AC Q923Y7;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE Trace amine receptor 2.
 GN TA2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=21374364; PubMed=11459929;
 RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
 RA Ogazalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
 RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
 RA Branche T.A., Gerald C.;
 RT "Trace amines: Identification of a family of mammalian G protein-
 coupled receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF180188; AAK71239.1; .
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro; IPR001000; Glyco hydro 10.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00591; GLYCOSYL HYDROL F10; 1.
 DR PROSITE; PS00237; G PROTEIN RECEPT F1 1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPT F1 2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 347 AA; 38783 MW; 86294B2876618B9 CRC64;

Query Match 51.5%; Score 927.5; DB 11; Length 347;
 Best Local Similarity 50.9%; Pred. No. 4.6e-78;
 Matches 168; Conservative 64; Mismatches 97; Indels 1; Gaps 1;
 Qy 3 FCNINISCVKXNNDVRSIYSLMLVLIITLVGNLIVIVISHPKQLHPTNWLH 62
 Db 14 FCFAAANNCPKRPALVVCAMYLVMIGAVMTLGNMVMVVISIAHFKQLHSPTNFLIL 73
 Qy 63 SMATVDFLLGCLVMPYSABHCWYFGVFCVCKHTSTDMILSSAIFHLISIDRY 122
 Db 74 SMATVDFLLGCLVMPYSABHCWYFGVFCVCKHTSTDMILSSAIFHLISIDRY 133
 Qy 123 AVCDDPLRYKAKMNLIVCMIFISWSVPVAFQGMIFLELNKGVBEIYRSQVSDLGG 182
 Db 134 AVCDDPLRYKAKMNLIVCMIFISWSVPVAFQGMIFLELNKGVBEIYRSQVSDLGG 192

Qy 193 VFFESKISGLVTEMTSPYIPQSIMLCVYRYIYLIAKEQARLISDANKLQIGLEMKNGISQ 242
 Db 193 LIFNKLWGLVASFIAFFLPGAIMVGIYIHFIVAKHARKIGPGRTRALSESXMKATS 252
 Qy 243 SKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 302
 Db 253 GKESKATKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 312
 Qy 303 YAFFYFVWFRKALKMFLGKIFQKDSRSRCKL 332
 Db 313 YGMFYFVWFRKALKMFLGKIFQKDSRSRCKL 342

RESULT 7

Q9P1P5 ID Q9P1P5 PRELIMINARY; PRT; 306 AA.
 AC Q9P1P5;
 DT 01-OCT-2000 (TremBLrel. 15, Created)
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE G-protein-coupled receptor 58.
 GN GPR58.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20149852; PubMed=10684976;
 RA Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,
 RA Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
 RA Marchese A.;
 RT "Cloning and characterization of additional members of the G protein-
 coupled receptor family.";
 RL Biochim. Biophys. Acta 1490:311-323(2000).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF112460; AAF27278.1; .
 DR Genew; HGNC:4514; GPR58.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G PROTEIN RECEPT F1 1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPT F1 2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 306 AA; 34924 MW; 55629F613062777C CRC64;

Query Match 45.3%; Score 815; DB 4; Length 306;
 Best Local Similarity 50.0%; Pred. No. 1.2e-67;
 Matches 158; Conservative 48; Mismatches 86; Indels 24; Gaps 4;

Qy 25 LYSMLVLIITLVGNLIVIVISHPKQLHPTNWLHSMATVDFLLGCLVMPYSVRS 84
 Db 1 MYSFMAISPTITFGNLAMIIISYFKQLHPTNFLNLSMAITDFLLGCLVMPYSVRS 60
 Qy 85 EHCWYFGEVFCVCKHTSTDMILSSAIFHLISIDRYAVCDPLRYKAKMNLIVCMIF 144
 Db 61 ENCWYFGLAFCKIYYSFSLMISITIFHLCSVAIDRFALCYALYKLTITPVKRL 120
 Qy 145 ISNSVPAVAFQGMIFLELNKGVBEIYRSQVSDLGG 182
 Db 121 LCWSVPGAFAGFAVFEAYADGIEG-YDILVACSSCPVMFNKLWGLTFMAAGFFTPGSM 179
 Qy 205 MLCVYRYIYLIAKEQARLISD--ANKLQIGLEMKNGISOSKERKAVKTLGIWGVFLIC 262
 Db 180 MCVGIYKGFVSKRHAHAINLNENQNV-----KKKKAAKTGIWGVFLIC 229
 Qy 263 WCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 302


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Db 230 WPCFTTLLDPLNFSTFWLFDALTWEGYFNSCNPLIYGGFFFWFRALKYILLGKI 289
QY 323 F-----OKDS 327
Db 290 FSSCFHTILCMQKES 305

RESULT 8
Q9P1P4 PRELIMINARY; PRT; 343 AA.
AC Q9P1P4
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE G protein-coupled receptor 57.
GN GPR57.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149852; PubMed=10684976;
RA Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,
RA Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
RA Marchese A.
RT "Cloning and characterization of additional members of the G protein-
coupled receptor family."
RL Biochim. Biophys. Acta 1490:311-323(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; AF112461; AAF27279.1; -.
DR Genbank; HGNC:4513; GPR57.
DR GO; GO:0036021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 343 AA; 39065 MW; DC513D15ABBC026F CRC64;

Query Match 45.2%; Score 813.5; DB 4; Length 343;
Best Local Similarity 46.0%; Pred. No. 1.8e-67;
Matches 159; Conservative 57; Mismatches 99; Indels 31; Gaps 5;

QY 4 CHNIN-----ISCVKN-----NSNDVRASLYSLMVLIIITLVGNLIVIVSISH 49
Db 13 CPKFNKILSSHQPLFCGDNVFGYDWSHY-----PLFGNLVIMVSISH 58
QY 50 FKQLHTPTNWLHSMATVDFLLGCLVMPYSVRSAEHCWYFGEVCKHTSTIDMLSSAS 109
Db 59 FKQLHSPNELLNATVDFLLGFMVYSIMRSVSCWYFGDGCKHTSFDMLRLTS 118
QY 110 IFHLSFTSIDRYAVCDPLRYAKKNILVICMIFISWSVPAVAFGMIFLELNPKGAE 169
Db 119 IFHLCISAIIDRFYAVCYPLHYTHYTKNTSTIKQLAFCSVPALFSGFLVSEADVSGMQS 178
QY 170 IYKHVHCRGCSVPSFKISGLVTWMTSFIYIPGSLMVCVYRIYLIKEQARLISDANOK 229
Db 179 -YKILVACNFCALTFNFWGTILFTTCFFPGSIMVGIYKIFTVSKOHARVISHPEN 237
QY 230 LQIGLEMKNGISQSKERKAVKTLGLVMGVFLICWCPFFICTWMPDPLHYIIPPTLVN 289
Db 238 TKGA--VKHLKSKKDKRAKTLGLVMGVFLACWLPCLFVLIDPDYDSTPILIDLV 295
QY 290 WFGYLNSTFNMVYAFFYVFWFRKALKMFLGKIFOKDSRRCKLFLE 335
Db 296 WLYRFNSTCNPLIHGFFNFWQKAFKYIVSGKIFSSHSETANLFPD 341
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RESULT 9
Q923Y6 PRELIMINARY; PRT; 338 AA.
AC Q923Y6
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Trace amine receptor 3.
GN TA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branche T.A., Gerald C.
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; AF380190; AAK71241.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 338 AA; 37846 MW; FBBC058A21664EA4 CRC64;

Query Match 43.4%; Score 782; DB 11; Length 338;
Best Local Similarity 45.8%; Pred. No. 1.5e-64;
Matches 154; Conservative 63; Mismatches 115; Indels 4; Gaps 4;

QY 1 MFCNIIINISCVKNNSNDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 60
Db 1 MELCVENVNGSCIKSSYSPWPRAILYAVLGLGALLAVFGLLVITAILHFQKLTPTN 60
QY 61 IHSMATVDFLLGCLVMPYSVRSAEHCWYFGEVCKHTSTIDMLSSASIFHLSFISIDR 120
Db 61 VASLACADFLVGTVMPESTVRSVEGVYFGDTYCKFTCTDTSFCFASLPHLCCISIDR 120
QY 121 YVAVCDPLRYAKKNILVICMIFISWSVPAVAFGMIFLELNPKGAEIYKHHVCRGG 180
Db 121 YVAVTDPLTYTKTISVSGVCIASLWFFSVTSYFSFYTGANEIGIELVVA-UTCVG 179
QY 181 CSVFFSKISGLVTWMTSFIYIPGSLMVCVYRIYLIKEQARLI--SDANQKLIQIGLEMKNG 239
Db 180 COAPLNQNWLLCFL--FFLPTVVMVFLYGRIFLVAQKQAKIEGSANQOASSSESYKER 238
QY 240 ISQSKERKAVKTLGLVMGVFLICWCPFFICTWMPDPLHYIIPPTLVNDFLWFGYLNSTFN 299
Db 239 VAR--RERKAATLGIAMAAFLVSWLPYIIDAVIDAYNFIPTPAYVYIELVWCVYNSAMN 297
QY 300 PMVYAFFYVFWFRKALKMFLGKIFOKDSRRCKLFLE 335
Db 298 PLIYAFFYVFWFRKALKLVSGKVFRASSSRNLFSF 333

RESULT 10
Q96RI9 PRELIMINARY; PRT; 348 AA.
ID Q96RI9
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GN TA7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhilani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheh T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380195; AAK71246.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_2; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 344 AA; 38043 MW; 45C41C961B5F6408 CRC64;

Query Match 40.7%; Score 733; DB 11; Length 344;
Best Local Similarity 41.2%; Pred. No. 5.7e-60;
Matches 139; Conservative 73; Mismatches 121; Indels 4; Gaps 3;

QY 1 MPFCHNIINISCVKNNWNSDVASISLMLVLIITLVGNLIVIVSISHFKQLHTPTNWL 60
DB 10 LQLCVENVASCKITPSPGLVLLYMWFGGAVLAVCGNLLVIVSLVHLKQLHSPANPL 69
QY 61 IHSMATVDFLLGLVMPYMSVRSABHCWYFGEVFCIKHTSTIDMLSSASIFHLSTISDR 120
DB 70 IASLASADFLVIGISWMPFSWVSIESCWYFGDTFCSLHSCDCAAFYCSLFLHCFISVDR 129
QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLEINFKGABEIIYKHVCRGG 180
DB 130 YIAVTEPLVYPTKFTMSVSGICISISWILPLVYSAVFTGISATGIENL-VSALNCVGG 188
QY 181 CSQSKERKAVKTLGIVMGVFLICWCPFFICTWMDPFLHYIIPPTLNDVLIWFGYLNSTF 238
DB 189 COVAINQDWLISFL-FPIPTLVMIILYSKILFLVAKQAVKIETISGSGKSSLESCHK 247
QY 239 GISQSKERKAVKTLGIVMGVFLICWCPFFICTWMDPFLHYIIPPTLNDVLIWFGYLNSTF 298
DB 248 ARVAKRERKAATLGVTVMAFWVSMPLTYTIDLDAFMGFTIPAVVYIEICGWIYNSAM 307
QY 299 NPMVYAFYFPFRKALKMMLFGKIFQKDSRCKLFLE 335
DB 308 NPLIYAFYFPFRKALKILSGKILKHSSTTSLSFE 344

RESULT 13
Q223Y5
ID Q223Y5 PRELIMINARY; PRT; 345 AA.
AC Q223Y5;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Trace amine receptor 4.
GN TA7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhilani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheh T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380191; AAK71242.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 345 AA; 38311 MW; DC904127D5B406EC CRC64;

Query Match 40.6%; Score 732; DB 11; Length 345;
Best Local Similarity 42.1%; Pred. No. 7.1e-60;
Matches 141; Conservative 65; Mismatches 127; Indels 2; Gaps 2;

QY 1 MPFCHNIINISCVKNNWNSDVASISLMLVLIITLVGNLIVIVSISHFKQLHTPTNWL 60
DB 11 LQLCVENVGSCVTPSPGPRVLLYAVFGGAVLAVFGNLLVIMISILHFKQLHSPTNFL 70
QY 61 IHSMATVDFLLGLVMPYMSVRSABHCWYFGEVFCIKHTSTIDMLSSASIFHLSTISDR 120
DB 71 IASLACADFWGVSWMPFSWVSIESCWYFGSFCFTFTCCDVAFCYSLFHLSTISDR 130
QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLEINFKGABEIIYKHVCRGG 180
DB 131 YIAVTDPLVYPTKFTVSGICISISWILPLAYSAVFTGVYADGLEEV-SDAVNCVGG 189
QY 181 CSVFSKISGVLTFTMSVFIPIGSMILCVYRIYLIYAKQARLISDANKLQIGLEMKGI 240
DB 190 COVVVYQ-NWVLIDFLSLIPTLVMIILYGNIFLVARQAKKIETVGNKAESSESSEYKAR 248
QY 241 SOSKERKAVKTLGIVMGVFLICWCPFFICTWMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 249 VARRERKAAKTIGITVAVAFMISWLEYSIDSLVDAFMGFTIPAYIYIEICVWCAYNSAMP 308
QY 301 MYVAFYFPFRKALKMMLFGKIFQKDSRCKLFLE 335
DB 309 LIYALFYFPFRKALKIVMSGVFNKSSATNLFSE 343

RESULT 14
Q223X9
ID Q223X9 PRELIMINARY; PRT; 374 AA.
AC Q223X9;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Trace amine receptor 11.
GN TA11.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;

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RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artyushyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380198; AAK71249.1; -.
DR GO; GO:00016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR Rhodopsn.
DR InterPro; IPR000585; Hemopexin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 374 AA; 41495 MW; C88FFDE2D04AA7AB CRC64;

Query Match 40.6%; Score 731; DB 11; Length 374;
Best Local Similarity 40.9%; Pred. No. 9.6e-60;
Matches 138; Conservative 72; Mismatches 123; Indels 4; Gaps 3;

QY 1 MPFCNINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
40 LQLCYENVNASCITKPYSGRLVLLVMVFGFGLAVLAVGNLIVISLVHFKQLHSPANFL 99
QY 61 IHSMATVDFLLGCLVMPYSWRSABHCWYFGVFCIKHTSTDIMLSSAIFHLSFISIDR 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
100 TASLASADFLVGISVMPFSWRSIESWCYFGDTFGLSCDAAFCYSSFLHLCFISVDR 159
QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPAYFAFGMIFLELNFKAEEIYYKHVHCRGG 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
160 YIATVDFLVPTKFTVSVSGICISISWILPLVYSSAVFTYGTISATGIENL-VSALNCVGG 218
QY 181 CSVFESKISGVLTFMTSYIPGIMLCVYRYIYLIJAKEQARLI--SDANQKLIQIGLEMKN 238
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
219 CQIVVQNDWLIDFL-FLIPTLVMLIYKIFLVAQKQAVKIETSISSKGESSLESHK 277
QY 239 GISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTINDVLIWFGYLNSTF 298
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
278 ARVAKRERKAATLGVTVAFVMSWLPYITDILDAFMGFITPAYVYEICCSWYNSAM 337
QY 299 NPMVYAFYPPWRKAKMMLFGKIFQKDSRCKLFLE 335
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
338 NPLIYAFYPPWRKAKILSGEILKSHSSTWSLFSF 374

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RESULT 15
Q923Y0 PRELIMINARY; PRT; 344 AA.
ID Q923Y0;
AC Q923Y0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Trace amine receptor 10.
GN TA10.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artyushyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,

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RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380198; AAK71249.1; -.
DR GO; GO:00016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR Rhodopsn.
DR InterPro; IPR000585; Hemopexin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 344 AA; 38015 MW; 6AB7A52CE3BEB692 CRC64;

Query Match 40.5%; Score 730; DB 11; Length 344;
Best Local Similarity 41.2%; Pred. No. 1.1e-59;
Matches 139; Conservative 71; Mismatches 123; Indels 4; Gaps 3;

QY 1 MPFCNINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
10 LQLCYENVNASCITKPYSGRLVLLVMVFGFGLAVLAVGNLIVISLVHFKQLHSPANFL 69
QY 61 IHSMATVDFLLGCLVMPYSWRSABHCWYFGVFCIKHTSTDIMLSSAIFHLSFISIDR 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
70 TASLASADFLVGISVMPFSWRSIESWCYFGDTFGLSCDAAFCYSSALHLCFISVDR 129
QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPAYFAFGMIFLELNFKAEEIYYKHVHCRGG 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
130 YIATVDFLVPTKFTVSVSGICISISWILPLVYSSAVFTYGTISATGIENL-VSALNCVGG 188
QY 181 CSVFESKISGVLTFMTSYIPGIMLCVYRYIYLIJAKEQARLI--SDANQKLIQIGLEMKN 238
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
189 CQIVVQNDWLISFL-FFIPTLVMLIYKIFLVAQKQAVKIETSVSGKGESSLESHK 247
QY 239 GISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTINDVLIWFGYLNSTF 298
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
248 ARVAKRERKAATLGVTVAFVMSWLPYITDILDAFMGFITPAYVYEICCSWYNSAM 307
QY 299 NPMVYAFYPPWRKAKMMLFGKIFQKDSRCKLFLE 335
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
308 NPLIYAFYPPWRKAKILSGILKSHSSTWSLFSF 344

```

Search completed: October 8, 2004, 10:20:55
Job time : 47 secs

FT Domain 287..307
 FT /note= "transmembrane domain 7"
 FT Modified-site 295..298
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 327..329
 FT /note= "Ser is O-phosphorylated by protein kinase C"
 XX
 PN WO200172841-A2.
 XX
 PD 04-OCT-2001.
 XX
 XX 27-MAR-2001; 2001WO-US009660.
 XX
 XX 27-MAR-2000; 2000US-0192311P.
 PR
 PR 04-AUG-2000; 2000US-00633145.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Kodira C, Cravchik A, Di Francesco V, Beasley EM;
 PI
 XX WPI; 2001-611617/70.
 DR N-PSDB; AAH26919, AAH26919.
 XX
 XX New human G-protein coupled receptor, useful for identifying specific
 PT modulators, potential therapeutic agents, is related to the aminergic
 PT receptor family.
 PT
 XX Claim 1; Fig 2; 60pp; English.
 PS
 CC The present sequence is that of a novel human G protein coupled receptor
 CC (GPCR) that is related to aminergic receptor family. GPCRs, particularly
 CC members of the aminergic receptor family, are a major target for drug
 CC action and development. The GPCR polypeptides and polynucleotides of the
 CC invention are therefore useful for the development of human therapeutic
 CC targets, can aid in the identification of therapeutic proteins, and serve
 CC as targets for the development of human therapeutic agents. The present
 CC GPCR is expressed in foetal brain, brain, placenta, liver, stomach and
 CC kidney, and is involved in signal transduction pathways. By targeting an
 CC agent to modulate the GPCR, the signalling activity and biological
 CC process mediated by the receptor can be agonised or antagonised in
 CC specific cells and tissues in order to modulate its biological activity
 CC in a therapeutic context (mammalian therapy) or toxic context (anti-cell
 CC therapy e.g. anti-cancer therapy)
 XX
 SQ Sequence 338 AA;
 Query Match 100.0%; Score 1801; DB 4; Length 338;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNWSDVRASLSYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 60
 Db 1 MPFCHNIINISCVKNNWSDVRASLSYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 60
 QY 61 IHSMATVDLGLCLVMPYSMVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 120
 Db 61 IHSMATVDLGLCLVMPYSMVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 120
 QY 121 YVAVCDPLRYKAKMNLIVICWIFISWSVPVAFGMIFLELNFKAEEIYKHHVCRGG 180
 Db 121 YVAVCDPLRYKAKMNLIVICWIFISWSVPVAFGMIFLELNFKAEEIYKHHVCRGG 180
 QY 181 CSVFFSKISGLVTFTSFYIPGIMLCVYIRYLIYLAKEQARLISDANQKIQIGLEMKNGI 240
 Db 181 CSVFFSKISGLVTFTSFYIPGIMLCVYIRYLIYLAKEQARLISDANQKIQIGLEMKNGI 240
 QY 241 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 Db 241 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 QY 301 MYAFYFPWFRKALKMFLGKIFQKDSRCKLPLELSS 338
 Db 301 MYAFYFPWFRKALKMFLGKIFQKDSRCKLPLELSS 338

RESULT 2
 AAB49232
 ID AAB49232 standard; protein; 339 AA.
 XX
 AC AAB49232;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human SNORF33 receptor protein.
 XX
 KW SNORF33; inflammation; arthritis; neurological disorder; infection;
 KW bone disease; respiratory disorder; asthma; cancer; cardiovascular.
 XX
 OS Homo sapiens.
 XX
 PN WO200073449-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US014654.
 XX
 PR 28-MAY-1999; 99US-00322257.
 PR 06-OCT-1999; 99US-00413433.
 XX
 XX (SYNA-) SYNAPTIC PHARM CORP.
 PA
 XX Borowsky BE, Ogozalek KL, Jones KA;
 PI
 XX WPI; 2001-025252/03.
 XX
 PT Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33 receptor
 PT which is useful for designing drugs for treating conditions such as a
 PT chronic and acute inflammation, arthritis, neurological disorders and
 PT microbial infections.
 XX
 PS Claim 9; Fig 6; 227pp; English.
 XX
 CC The present invention relates to a mammalian SNORF33 receptor. SNORF33
 CC antagonists and agonists are used to treat abnormalities brought about by
 CC increased or decreased activity of the mammalian SNORF33 receptor. The
 CC receptor is useful as a tool for designing drugs for treating conditions
 CC such as a chronic and acute inflammation, arthritis, neurological
 CC disorders, microbial infections, bone diseases, respiratory disorders
 CC such as asthma, cancers, cardiovascular disorders
 XX
 SQ Sequence 339 AA;
 Query Match 100.0%; Score 1801; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNWSDVRASLSYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 60
 Db 2 MPFCHNIINISCVKNNWSDVRASLSYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 61
 QY 61 IHSMATVDLGLCLVMPYSMVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 120
 Db 62 IHSMATVDLGLCLVMPYSMVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 121
 QY 121 YVAVCDPLRYKAKMNLIVICWIFISWSVPVAFGMIFLELNFKAEEIYKHHVCRGG 180
 Db 122 YVAVCDPLRYKAKMNLIVICWIFISWSVPVAFGMIFLELNFKAEEIYKHHVCRGG 181
 QY 181 CSVFFSKISGLVTFTSFYIPGIMLCVYIRYLIYLAKEQARLISDANQKIQIGLEMKNGI 240
 Db 182 CSVFFSKISGLVTFTSFYIPGIMLCVYIRYLIYLAKEQARLISDANQKIQIGLEMKNGI 241
 QY 241 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 Db 242 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301

QY 301 MYAFYFWRKALXKMLFGKIFQKDSRCKLFLELSS 338
 DB 302 MYAFYFWRKALXKMLFGKIFQKDSRCKLFLELSS 339

RESULT 3
 ID AAG80973 standard; protein; 339 AA.
 XX AAG80973;
 XX 28-AUG-2001 (first entry)
 XX Human nGPCR56 #3.
 XX G protein-coupled receptor; nGPCR; seven transmembrane receptor;
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KW neuroprotective.
 OS Homo sapiens.
 PN WO200136473-A2.
 XX 25-MAY-2001.
 XX 16-NOV-2000; 2000WO-US031581.
 XX 16-NOV-1999; 99US-0165838P.
 XX 17-NOV-1999; 99US-0166071P.
 XX 19-NOV-1999; 99US-0166678P.
 XX 28-DEC-1999; 99US-0173396P.
 XX 28-FEB-2000; 2000US-0184129P.
 XX 28-FEB-2000; 2000US-0185421P.
 XX 28-FEB-2000; 2000US-0185554P.
 XX 02-MAR-2000; 2000US-0186530P.
 XX 03-MAR-2000; 2000US-0186811P.
 XX 09-MAR-2000; 2000US-0190310P.
 XX 17-MAR-2000; 2000US-0190310P.
 XX 21-MAR-2000; 2000US-0190800P.
 XX 20-APR-2000; 2000US-0198568P.
 XX 02-MAY-2000; 2000US-0201190P.
 XX 08-MAY-2000; 2000US-0203111P.
 XX 25-MAY-2000; 2000US-0207094P.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PA Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
 FI Schellin KA, Kaytes PS, Bannigan CW, Ruff V, Sejlitz T, Huff RM;
 XX WPI; 2001-389826/41.
 XX N-PSDB; AAH51013.
 XX New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
 PT useful for diagnosing and treating e.g. schizophrenia.
 XX Claim 37; Page 92; 261pp; English.
 XX The present invention relates to novel G protein-coupled receptors
 CC (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
 CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
 CC one such G protein-coupled receptor. GPCRs are also known as seven
 CC transmembrane receptors and function in signal transduction. The nGPCR
 CC coding sequences are useful for screening a human to diagnose a disorder
 CC affecting the brain or a genetic predisposition, specifically
 CC schizophrenia. nGPCR are useful for identifying compounds useful for
 CC treating schizophrenia. Detection of nGPCR in a sample is useful as a
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal

CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
 CC metabolic and cardiovascular diseases, proliferative disorders and
 CC hormonal disorders. Modulators of nGPCR activity have the utility for
 CC treating neurological disorders, including schizophrenia, ADHD/ADD
 CC (attention deficit-hyperactivity disorder/attention deficit disorder),
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
 CC migraine and senile dementia. Additional disorders include inflammatory
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
 CC diseases e.g. inflammatory bowel disease
 XX Sequence 339 AA;
 SQ

Query Match 100.0%; Score 1801; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNNWSDYRASLYSLMWLIITLTVGNLIVIVSISHFKOLHPTNWL 60
 DB 2 MPFCHNIINISCVKNNWSDYRASLYSLMWLIITLTVGNLIVIVSISHFKOLHPTNWL 61
 QY 61 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 120
 DB 62 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 121
 QY 121 YYAVCDPLRYKAKNNILVICVMIFISWSVPAPAFGMIFLELNFKGABEIIYKHHVCRGG 180
 DB 122 YYAVCDPLRYKAKNNILVICVMIFISWSVPAPAFGMIFLELNFKGABEIIYKHHVCRGG 181
 QY 181 CSVFESKISGVLTFMTSFYIPGSIMLCVYRYIYLIAKEQARLISDANOKLQIGLEKNGI 240
 DB 182 CSVFESKISGVLTFMTSFYIPGSIMLCVYRYIYLIAKEQARLISDANOKLQIGLEKNGI 241
 QY 241 SQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPPLHYIIIPPTLNDVLIWFGYLNSTNP 300
 DB 242 SQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPPLHYIIIPPTLNDVLIWFGYLNSTNP 301
 QY 301 MYAFYFWRKALXKMLFGKIFQKDSRCKLFLELSS 338
 DB 302 MYAFYFWRKALXKMLFGKIFQKDSRCKLFLELSS 339

RESULT 4
 ABJ04073
 ID ABJ04073 standard; protein; 339 AA.
 XX ABJ04073;
 XX 11-OCT-2002 (first entry)
 XX Human G protein coupled receptor hrUP33.
 XX Human; G-protein coupled receptor; GPCR; hrUP28; hrUP29; hrUP30; hrUP31;
 KW hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37.
 XX Homo sapiens.
 XX WO200242461-A2.
 XX 30-MAY-2002.
 XX 26-NOV-2001; 2001WO-US044386.
 XX 27-NOV-2000; 2000US-0253404P.
 XX 12-DEC-2000; 2000US-0255366P.
 XX 20-FEB-2001; 2001US-0270266P.
 XX 20-FEB-2001; 2001US-0270286P.
 XX 06-APR-2001; 2001US-0282032P.
 XX 06-APR-2001; 2001US-0282356P.
 XX 06-APR-2001; 2001US-0282358P.
 XX 14-MAY-2001; 2001US-0290917P.
 XX 31-JUL-2001; 2001US-0309208P.

XX (AREN-) ARENA PHARM INC.
 XX Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
 XX WPI; 2002-566565/60.
 XX N-PSDB; ABT04871.
 XX Novel endogenous and non-endogenous versions of G protein-coupled
 PT receptor useful for identification of candidate compounds as receptor
 PT agonists or antagonists for use as therapeutic agents.
 XX Claim 21; Page 66-67; 84pp; English.
 XX The present invention provides the protein and coding sequences of
 CC several human G-protein coupled receptors (GPCRs). These can be used in
 CC the identification of candidate compounds as receptor agonists or inverse
 CC agonists having applicability as therapeutic agents. The present sequence
 CC is a GPCR protein of the invention
 XX Sequence 339 AA;
 SQ
 Query Match 100.0%; Score 1801; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNNSNDVRASLYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 60
 Db 2 MPFCHNIINISCVKNNNSNDVRASLYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 61
 QY 61 IHSMATVDPLLGCLVMPYSWVRSACHWVFGVFCCKIHTSTDIMLSSASIFHLSFISIDR 120
 Db 62 IHSMATVDPLLGCLVMPYSWVRSACHWVFGVFCCKIHTSTDIMLSSASIFHLSFISIDR 121
 QY 121 YVAVCDPLRYKAKNNILVICVMIFISWSVPAVAFGMIFLELNFPGABEIIYKHHVCRGG 180
 Db 122 YVAVCDPLRYKAKNNILVICVMIFISWSVPAVAFGMIFLELNFPGABEIIYKHHVCRGG 181
 QY 181 CSVFFSKISGVLTFMTSTYIPGSIIMLCVYRYIYLAKQARLISDANQKLGLEWKNKI 240
 Db 182 CSVFFSKISGVLTFMTSTYIPGSIIMLCVYRYIYLAKQARLISDANQKLGLEWKNKI 241
 QY 241 SOSKERKAVKTLGIVMGVFLICWCPCFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 Db 242 SOSKERKAVKTLGIVMGVFLICWCPCFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
 QY 301 MYAIFYPWFPRKALKOMLFGKIFQKDSRCKLFLELSS 338
 Db 302 MYAIFYPWFPRKALKOMLFGKIFQKDSRCKLFLELSS 339
 RESULT 5
 ID ABG93791 standard; protein; 339 AA.
 XX AC ABG93791;
 XX DT 26-NOV-2002 (first entry)
 XX DE Human G protein-coupled receptor protein, nGPCR-56, #2.
 XX Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
 KW nGPCR protein coupled receptor; communication; serpentine structure;
 KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
 KW genetic predisposition; brain; immune response; gene therapy;
 KW anxiety disorder; depression; bipolar disorder; schizophrenia;
 KW Huntington's disease; dyskinesia; manic depression; stroke;
 KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
 KW tranquiliser.
 XX OS Homo sapiens.
 XX WO200264789-A1.
 PN

XX 22-AUG-2002.
 XX 14-FEB-2001; 2001WO-US004641.
 XX 14-FEB-2001; 2001WO-US004641.
 XX (PHMA) PHARMACIA & UPTJOHN CO.
 XX Lind P, Parodi LA, Vogeli G, Wood LS;
 XX WPI; 2002-674879/72.
 XX N-PSDB; ABS70246.
 XX New nucleic acids and polypeptides of the nG protein-coupled receptor,
 PT useful for treating or diagnosing a mental disorder or a disorder
 PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
 PT Parkinson's disease.
 XX Example 1; Page 87; 244pp; English.
 XX The invention discloses an isolated human polypeptide, and encoding
 CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
 CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
 CC communication between cells and their environment and are characterised
 CC by a serpentine structure that passes through the cell membrane seven
 CC times, hence the reason such receptors are sometimes called seven
 CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
 CC useful for identifying an nGPCR allelic variant that correlates with a
 CC mental disorder, for isolating an antibody that binds to an epitope of
 CC the polypeptide, for identifying a compound that binds the polypeptide or
 CC polynucleotide and/or modulates its biological activity, for screening a
 CC human subject to diagnose a disorder, or a genetic predisposition to a
 CC disorder, affecting the brain or a genetic disposition to the disorder,
 CC for identifying compounds useful for the treatment of a mental disorder
 CC and for identifying a compound useful as a modulator of binding between
 CC nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also
 CC useful for inducing an immune response in a mammal. The nucleic acid or
 CC polypeptide is particularly useful, using gene therapy, for treating e.g.
 CC anxiety disorders, depression, bipolar disorder, schizophrenia,
 CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
 CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
 CC be used for treating diabetes, inflammation or wounds. The sequences
 CC presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nGPCR (also
 CC referred to as beGPCRs) proteins
 XX SQ Sequence 339 AA;
 Query Match 100.0%; Score 1801; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNNSNDVRASLYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 60
 Db 2 MPFCHNIINISCVKNNNSNDVRASLYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 61
 QY 61 IHSMATVDPLLGCLVMPYSWVRSACHWVFGVFCCKIHTSTDIMLSSASIFHLSFISIDR 120
 Db 62 IHSMATVDPLLGCLVMPYSWVRSACHWVFGVFCCKIHTSTDIMLSSASIFHLSFISIDR 121
 QY 121 YVAVCDPLRYKAKNNILVICVMIFISWSVPAVAFGMIFLELNFPGABEIIYKHHVCRGG 180
 Db 122 YVAVCDPLRYKAKNNILVICVMIFISWSVPAVAFGMIFLELNFPGABEIIYKHHVCRGG 181
 QY 181 CSVFFSKISGVLTFMTSTYIPGSIIMLCVYRYIYLAKQARLISDANQKLGLEWKNKI 240
 Db 182 CSVFFSKISGVLTFMTSTYIPGSIIMLCVYRYIYLAKQARLISDANQKLGLEWKNKI 241
 QY 241 SOSKERKAVKTLGIVMGVFLICWCPCFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 Db 242 SOSKERKAVKTLGIVMGVFLICWCPCFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
 QY 301 MYAIFYPWFPRKALKOMLFGKIFQKDSRCKLFLELSS 338
 PN

||||| 302 MYAIFYPWFPRKALXWMLFGKIFQKDSRCKLFLELSS 339

RESULT 6

ABP81732
ID ABP81732 standard; protein; 339 AA.

AC ABP81732;

DT 04-MAR-2003 (first entry)

DE Human trace amine receptor 1 protein SEQ ID NO:639.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor; modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer.

XX Homo sapiens.

OS WO200261087-A2.

PN 08-AUG-2002.

PD 19-DEC-2001; 2001WO-US050107.

PF 19-DEC-2000; 2000US-0257144P.

PR (LIFE-) LIFESPAN BIOSCIENCES INC.

PA Burner GC, Roush CL, Brown JP;

PI WPI; 2003-046718/04.

DR N-PSDB; AB242578.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode

CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX SQ Sequence 339 AA;

Query Match 100.0%; Score 1801; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 4.3e-199;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSNDVRASLYSLMVLIIITLVGNLIIVIVISHSFKQLHTPTNWL 60
Db |||||||

QY 2 MPFCHNIINISCVKNWNSNDVRASLYSLMVLIIITLVGNLIIVIVISHSFKQLHTPTNWL 61
Db |||||||

QY 61 IHSMATVDLGLCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDMLSASIFHLSPFISDR 120
Db |||||||

QY 62 IHSMATVDLGLCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDMLSASIFHLSPFISDR 121
Db |||||||

QY 121 YVAVCDPLRYKAKNNILVICVMIFISWSVPVAFAGMIFLELNFKGAETIYKGVHCRGG 180
Db |||||||

QY 122 YVAVCDPLRYKAKNNILVICVMIFISWSVPVAFAGMIFLELNFKGAETIYKGVHCRGG 181
Db |||||||

QY 181 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYIRIYLIATKEQARLISDANQKLGLEMKNGI 240
Db |||||||

QY 182 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYIRIYLIATKEQARLISDANQKLGLEMKNGI 241
Db |||||||

QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPLHYIIPPTLNDVLWFGYLNSTFNP 300
Db |||||||

QY 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPLHYIIPPTLNDVLWFGYLNSTFNP 301
Db |||||||

QY 301 MYAIFYPWFPRKALXWMLFGKIFQKDSRCKLFLELSS 338
Db |||||||

QY 302 MYAIFYPWFPRKALXWMLFGKIFQKDSRCKLFLELSS 339
Db |||||||

RESULT 7

ABP80694

ID ABB80694 standard; protein; 339 AA.

AC ABB80694;

XX 15-JUL-2002 (first entry)

DT Human trace amine receptor.

DE Biogenic receptor; trace amine receptor; synaptic transmission; human;
XX hyperthermia; blood pressure; migraine; cardiac arrhythmia; seizure;
XX coma; diabetes; schizophrenia; hypertension; asthma; drug addiction.

XX Homo sapiens.

XX WO200222801-A2.

XX 21-MAR-2002.

XX 12-SEP-2001; 2001WO-US028455.

XX 12-SEP-2000; 2000US-00659519.

XX 09-JUL-2001; 2001US-0303967P.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Bunzow JR, Grandy DK, Sonders M;

XX WPI; 2002-371971/40.

XX N-PSDB; ABL58316.

XX A novel mammalian biogenic amine receptor, useful in assays to identify
XX therapeutic agents for treating e.g., asthma and shock.
XX Claim 4; Fig 1; 86pp; English.

XX The invention relates to novel mammalian (human and rat) biogenic amine
XX receptors. The mammalian biogenic receptors can be used to screen for

CC compounds that bind to it, or to screen for compounds that inhibit a
 CC mammalian trace amine receptor. The compounds identified by the assay
 CC amine dependent synaptic transmission in mammals so they can be used to
 CC to treat the peripheral effects of a drug that binds to or affects the
 CC binding to trace amine receptors e.g. hyperthermia, rapid heart rate,
 CC high blood pressure, migraine, cardiac arrhythmia, seizure, coma and
 CC diabetes or to treat pathological conditions associated with elevated
 CC levels of trace amines e.g. schizophrenia, depression, hypertension,
 CC shock, cardiac arrhythmias, asthma, migraine, psychosis, anaphylactic
 CC reactions and iatrogenic conditions. They are also useful for treating
 CC drug addiction. The present sequence represents a human trace amine
 CC receptor

XX Sequence 339 AA;

SQ
 Query Match 99.2%; Score 1786; DB 5; Length 339;
 Best Local Similarity 99.4%; Pred. No. 2.3e-197;
 Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFPCNNINISCVKNWSDVRSLSYSLMVLIIITLVGNLIVIVSISHFQKQLHTPTNWL 60
 DB 2 MFPCNNINISCVKNWSDVRSLSYSLMVLIIITLVGNLIVIVSISHFQKQLHTPTNWL 61
 QY 61 IHSMATVDFLLGLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSPISIDR 120
 DB 62 IHSMATVDFLLGLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSPISIDR 121
 QY 121 YVAVCDPLRYKAKNNILVICVMIFISWSVPAVPAFGMIFLELNFKGAEEIYKHVHCRCG 180
 DB 122 YVAVCDPLRYKAKNNILVICVMIFISWSVPAVPAFGMIFLELNFKGAEEIYKHVHCRCG 181
 QY 181 CSVFSKISGLVTFMTSPFIPGSLMVCVYRIYLIKEQARLISDANQKLGLEMKNGI 240
 DB 182 CLVFFSKISGLVTFMTSPFIPGSLMVCVYRIYLIKEQARLISDANQKLGLEMKNGI 241
 QY 241 SOSKERKAVTKTIGLVNGVFLICWCPFFICTVMDPFLHIIPTLNDVLVWFGYLNSTFNP 300
 DB 242 SOSKERKAVTKTIGLVNGVFLICWCPFFICTVMDPFLHIIPTLNDVLVWFGYLNSTFNP 301
 QY 301 MYVAFYPWFRKALKWMLFGKIFQKDSRCKLFLSS 338
 DB 302 MYVAFYPWFRKALKWMLFGKIFQKDSRCKLFLSS 339

RESULT 8
 ADC12792
 ID ADC12792 standard; protein; 311 AA.

XX ADC12792;
 AC
 XX 18-DEC-2003 (first entry)
 DT
 XX Human GPCR protein, SEQ ID No 124.
 DE
 XX G protein-coupled receptor; GPCR; antibacterial; fungicide; protozoacide;
 KW virucide; antirheumatic; antiarthritic; tranquiliser; antidiabetic;
 KW osteopathic; neurotropic; neuroprotective; anorectic; cardiant;
 KW neuroleptic; cytostatic; antiparkinsonian; hypotensive; hypertensive;
 KW antitumor; antiallergic; anticonvulsant; analgesic; infection;
 KW rheumatoid arthritis; chronic obstructive pulmonary diseases; COPD;
 KW asthma; non-insulin dependent diabetes; obesity; osteoporosis;
 KW Alzheimer's disease; age-related macular degeneration;
 KW myocardial infarction; schizophrenia; osteoarthritis; cancer;
 KW Parkinson's disease; congestive heart failure; hypotension; hypertension;
 KW ulcer; benign prostatic hyperplasia; seizure disorder; anxiety;
 KW obsessive compulsive disorder; Cushing's syndrome; hypopituitarism; pain;
 KW human.
 XX Homo sapiens.
 OS
 XX WO2003000893-A2.
 PN
 XX

PD 03-JAN-2003.
 XX
 PP 24-JUN-2002; 2002WO-IB002357.
 XX
 PR 26-JUN-2001; 2001US-0301095P.
 PR 06-NOV-2001; 2001US-0333185P.
 XX
 PA (DECO-) DECODE GENETICS EHF.
 XX
 XX Martinez RMA, Sigurdsson GT;
 PI WPI; 2003-210155/20.
 DR N-PSDB; ADC12791.
 XX
 PT New G protein-coupled receptor (GPCR) genes and polypeptides, useful for
 PT diagnosing diseases associated with a GPCR, or in gene therapy for
 PT treating e.g. obesity, osteoporosis, Alzheimer's, cancers or congestive
 PT heart failure.
 XX
 PS Claim 10; SEQ ID NO 124; 253pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid of a G protein-
 CC coupled receptor (GPCR) gene comprising any of 62 sequences of 912-2454
 CC bp, or its complements; a GPCR polypeptide comprising any of 62 sequences
 CC of 291-818 amino acids; or a nucleic acid that hybridises, under high
 CC stringency conditions, with any of the 62 GPCR sequences or any of their
 CC complements. The GPCR agents of the invention have the following
 CC activities: antibacterial, fungicide, protozoacide, virucide,
 CC antirheumatic, tranquiliser, antiarthritic, antidiabetic, osteopathic,
 CC neuroleptic, neuroprotective, anorectic, cardiant, neuroleptic, cyostatic,
 CC antiparkinsonian, hypotensive, hypertensive, antitumor, antiallergic,
 CC anticonvulsant, and analgesic. The GPCR therapeutic agent, particularly a
 CC GPCR gene agonist or antagonist, is useful for treating a disease or
 CC condition associated with a GPCR in an individual. The nucleic acid cited
 CC above, which is 100 or fewer nucleotides in length, is useful for
 CC assaying a sample for the presence of the GPCR gene nucleic acid or a
 CC GPCR gene nucleic acid with at least one nucleotide difference from a
 CC first nucleic acid, or for diagnosing a susceptibility to a disease or
 CC conditions associated with a GPCR. These diseases include infections
 CC (e.g. bacterial, fungal, protozoan or viral), rheumatoid arthritis,
 CC chronic obstructive pulmonary diseases (COPD), asthma, non-insulin
 CC dependent diabetes, obesity, osteoporosis, Alzheimer's disease, age-
 CC related macular degeneration, myocardial infarction, schizophrenia,
 CC osteoarthritis, cancers, Parkinson's diseases, congestive heart failure,
 CC hypertension, hypotension, ulcers, allergies, benign prostatic
 CC hyperplasia, seizure disorder, anxiety, obsessive compulsive disorder,
 CC Cushing's syndrome, hypopituitarism, or pain. This sequence represents
 CC one of the 62 GPCR proteins of the invention.
 XX
 XX Sequence 311 AA;

Query Match 85.5%; Score 1539; DB 7; Length 311;
 Best Local Similarity 100.0%; Pred. No. 7.5e-169;
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 LMVLIITLVGNLIVIVSISHFQKQLHTPTNWLHSMATVDFLLGLVMPYSWVSAEHC 87
 DB 23 LMVLIITLVGNLIVIVSISHFQKQLHTPTNWLHSMATVDFLLGLVMPYSWVSAEHC 82
 QY 88 WYFGEVFCIKHTSTDMILSSASIFHLSPISIDRYAVCDPLRYKAKNNILVICWIFISW 147
 DB 83 WYFGEVFCIKHTSTDMILSSASIFHLSPISIDRYAVCDPLRYKAKNNILVICWIFISW 142
 QY 148 SYPVAFAGMIFLELNFKGAEEIYKHVHCRCGSVFFSKISGLVTFMTSPFIPGSLMCL 207
 DB 143 SYPVAFAGMIFLELNFKGAEEIYKHVHCRCGSVFFSKISGLVTFMTSPFIPGSLMCL 202
 QY 208 VYVRIYLIKEQARLISDANQKLGLEMKNGISQSKERKAVTKLTVGMVFLICWCPFF 267
 DB 203 VYVRIYLIKEQARLISDANQKLGLEMKNGISQSKERKAVTKLTVGMVFLICWCPFF 262
 QY 268 ICTVMDPFLHIIPTLNDVLVWFGYLNSTFNPVYAFYFWRKALKM 316

DB 263 ICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNDVMVYAFYFPERKALKM 311

RESULT 9

AAG80972

ID AAG80972 standard; protein; 296 AA.

AC AAG80972;

XX

DT 28-AUG-2001 (first entry)

XX

DE Human nGPCR56 #2.

XX

XX G protein-coupled receptor; nGPCR; seven transmembrane receptor;

KW signal transduction; schizophrenia; thyroid disorder; renal failure;

KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;

KW cardiovascular disease; proliferative disorder; hormonal disease;

KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;

KW attention deficit-hyperactivity disorder/attention deficit disorder;

KW Parkinson's disease; migraine; senile dementia; inflammatory disease;

KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;

XX neuroprotective.

OS Homo sapiens.

XX

PN WO200136473-A2.

XX

PD 25-MAY-2001.

XX

PF 16-NOV-2000; 2000WO-US031581.

XX

PR 16-NOV-1999; 99US-0165838P.

PR 17-NOV-1999; 99US-0166071P.

PR 19-NOV-1999; 99US-0166678P.

PR 28-DEC-1999; 99US-0173396P.

PR 22-FEB-2000; 2000US-0184129P.

PR 28-FEB-2000; 2000US-0185421P.

PR 28-FEB-2000; 2000US-0185554P.

PR 02-MAR-2000; 2000US-0186530P.

PR 03-MAR-2000; 2000US-0186811P.

PR 09-MAR-2000; 2000US-0188114P.

PR 17-MAR-2000; 2000US-0190310P.

PR 21-MAR-2000; 2000US-0190800P.

PR 20-APR-2000; 2000US-0198568P.

PR 02-MAY-2000; 2000US-0201190P.

PR 08-MAY-2000; 2000US-0203111P.

PR 25-MAY-2000; 2000US-0207094P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Vogeli G, Wood LS, Parodi LA, Hiebach RR, Lind P, Slightom J;

PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;

XX

DR WPI; 2001-389826/41.

DR N-PSDB; AAH51012.

XX

PT New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide

XX useful for diagnosing and treating e.g. schizophrenia.

PS Claim 37; Page 91-92; 261pp; English.

XX

CC The present invention relates to novel G protein-coupled receptors

CC (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,

CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is

CC one such G protein-coupled receptor. GPCRs are also known as seven

CC transmembrane receptors and function in signal transduction. The nGPCRx

CC coding sequences are useful for screening a human to diagnose a disorder

CC affecting the brain or a genetic predisposition, specifically

CC schizophrenia. nGPCRx are useful for identifying compounds useful for

CC treating schizophrenia. Detection of nGPCRx in a sample is useful as a

CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal

CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,

CC metabolic and cardiovascular diseases, proliferative disorders and

CC

CC hormonal disorders. Modulators of nGPCRx activity have the utility for

CC treating neurological disorders, including schizophrenia, ADHD/ADD

CC (attention deficit-hyperactivity disorder/attention deficit disorder),

CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,

CC migraine and senile dementia. Additional disorders include inflammatory

CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune

CC disorders, cancers, respiratory ailments such as asthma, and inflammatory

XX diseases e.g. inflammatory bowel disease

SQ Sequence 296 AA;

Query Match 84.4%; Score 1520; DB 4; Length 296;

Best Local Similarity 100.0%; Pred. No. 1,1e-166; Indels 0; Gaps 0;

Matches 286; Conservative 0; Mismatches 0;

QY 1 MPFCHNIINISCVKNNWSNDVRASLYSLMVLIIITLVGNLIVIVISHSFKQLHTPTNWL 60

DB 2 MPFCHNIINISCVKNNWSNDVRASLYSLMVLIIITLVGNLIVIVISHSFKQLHTPTNWL 61

QY 61 IHSMATVDLGLCLVMPYSMVRSASAEHCWYFGEVFCIKHTSTOIMLSSASIFHLSPFISDR 120

DB 62 IHSMATVDLGLCLVMPYSMVRSASAEHCWYFGEVFCIKHTSTOIMLSSASIFHLSPFISDR 121

QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFGMIFELNFKGAETIYKHHVHCRGS 180

DB 122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFGMIFELNFKGAETIYKHHVHCRGS 181

QY 181 CSVFFSKISGVLTFMTSFYIPGSIMLCVYRIYLIKAQARLISDANQKLIQIGLEMKNGI 240

DB 182 CSVFFSKISGVLTFMTSFYIPGSIMLCVYRIYLIKAQARLISDANQKLIQIGLEMKNGI 241

QY 241 SOSKERKAVKTLGIYGVNVELICWCPFFICTVMDPFLHYIIPPTLND 286

DB 242 SOSKERKAVKTLGIYGVNVELICWCPFFICTVMDPFLHYIIPPTLND 287

RESULT 10

ABG93790

ID ABG93790 standard; protein; 296 AA.

XX

AC ABG93790;

XX

DT 26-NOV-2002 (first entry)

XX

DE Human G protein-coupled receptor protein, nGPCR-56, #1.

XX

KW Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;

KW nG protein coupled receptor; communication; serpentine structure;

KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;

KW genetic predisposition; brain; immune response; gene therapy;

KW anxiety disorder; depression; bipolar disorder; schizophrenia;

KW Huntington's disease; dyskinesia; manic depression; stroke;

KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;

KW tranquilliser.

XX

OS Homo sapiens.

XX

PN WO200264789-A1.

XX

PD 22-AUG-2002.

XX

PF 14-FEB-2001; 2001WO-US004641.

XX

PR 14-FEB-2001; 2001WO-US004641.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Lind P, Parodi LA, Vogeli G, Wood LS;

XX WPI; 2002-674879/72.

DR N-PSDB; ABS70245.

XX

PT New nucleic acids and polypeptides of the nG protein-coupled receptor,

PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
XX Parkinson's disease.

XX Example 1; Page 86-87; 244pp; English.

XX The invention discloses an isolated human polypeptide, and encoding
XX nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
CC ng protein coupled receptor-14 (ngPCR-14). GPCRs are vital in the
CC communication between cells and their environment and are characterised
CC by a serpentine structure that passes through the cell membrane seven
CC times, hence the reason such receptors are sometimes called seven
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
CC useful for identifying an nPCR allelic variant that correlates with a
CC mental disorder, for isolating an antibody that binds to an epitope of
CC the polypeptide, for identifying a compound that binds the polypeptide or
CC polynucleotide and/or modulates its biological activity, for screening a
CC human subject to diagnose a disorder, or a genetic predisposition to a
CC disorder, affecting the brain or a genetic disposition to the disorder,
CC for identifying compounds useful for the treatment of a mental disorder,
CC and for identifying a compound useful as a modulator of binding between
CC ngPCR-14 and a binding partner of ngPCR-14. The polypeptide is also
CC useful for inducing an immune response in a mammal. The nucleic acid or
CC polypeptide is particularly useful, using gene therapy, for treating e.g.
CC anxiety disorders, depression, bipolar disorder, schizophrenia,
CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
CC be used for treating diabetes, inflammation or wounds. The sequences
CC presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nPCR (also
CC referred to as bcGPCR) proteins

XX Sequence 296 AA;

Query Match 84.4%; Score 1520; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.1e-166;

Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCNIIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKQHTPTNWL 60
DB 2 MPFCNIIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKQHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSNVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFISIDR 120
DB 62 IHSMATVDFLLGCLVMPYSNVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFISIDR 121
QY 121 YVAVCDPLRYKAKWNTLVICVMIFISWSVPAPVAFGMIFELNFKGAEIYYKHVHCRGG 180
DB 122 YVAVCDPLRYKAKWNTLVICVMIFISWSVPAPVAFGMIFELNFKGAEIYYKHVHCRGG 181
QY 181 CSVFFSKISGVLTFMTSFYIPGIMLCVYRIYLIKEQARLISDANQKIQIGLEMKNGI 240
DB 182 CSVFFSKISGVLTFMTSFYIPGIMLCVYRIYLIKEQARLISDANQKIQIGLEMKNGI 241
QY 241 SQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLND 286
DB 242 SQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLND 287

RESULT 11

ID AAB49231
XX AAB49231 standard; protein; 332 AA.

XX AAB49231;

XX 14-MAR-2001 (first entry)

XX Rat SNORF33 receptor protein.

XX SNORF33; inflammation; arthritis; neurological disorder; infection;
XX bone disease; respiratory disorder; asthma; cancer; cardiovascular.

XX Rattus rattus.

XX

PN WO200073449-A1.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-USO14654.

XX 28-MAY-1999; 99US-00322257.

XX 06-OCT-1999; 99US-00413433.

XX (SYNA-) SYNAPTIC PHARM CORP.

XX Borowsky BE, Ogozalek KL, Jones KA;

XX WPI; 2001-025252/03.

XX Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33 receptor
PT which is useful for designing drugs for treating conditions such as a
PT chronic and acute inflammation, arthritis, neurological disorders and
PT microbial infections.

XX Claim 12; Fig 4; 227pp; English.

XX The present invention relates to a mammalian SNORF33 receptor. SNORF33
CC antagonists and agonists are used to treat abnormalities brought about by
CC increased or decreased activity of the mammalian SNORF33 receptor. The
CC receptor is useful as a tool for designing drugs for treating conditions
CC such as a chronic and acute inflammation, arthritis, neurological
CC disorders, microbial infections, bone diseases, respiratory disorders
CC such as asthma, cancers, cardiovascular disorders

XX Sequence 332 AA;

Query Match 77.9%; Score 1403; DB 4; Length 332;

Best Local Similarity 78.1%; Pred. No. 4.4e-153;

Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;

QY 1 MPFCNIIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKQHTPTNWL 60
DB 1 MHLCHNSANISHTNSNWSRDRASLYSLIILITLVGNLIVIVISHFQKQHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSNVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFISIDR 120
DB 61 LHSMAVVDLGLCLVMPYSNVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFISIDR 120
QY 121 YVAVCDPLRYKAKWNTLVICVMIFISWSVPAPVAFGMIFELNFKGAEIYYKHVHCRGG 180
DB 121 YVAVCDPLRYKAKWNTLVICVMIFISWSVPAPVAFGMIFELNFKGAEIYYKHVHCRGG 180
QY 181 CSVFFSKISGVLTFMTSFYIPGIMLCVYRIYLIKEQARLISDANQKIQIGLEMKNGI 240
DB 181 CFPFFSKVSGVLAFMTSFYIPGIMLCVYRIYLIKEQARLISDANQKIQIGLEMKNGI 238
QY 241 SQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVILWFGYLNSTFNP 300
DB 239 PQSKETKAAKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVILWFGYLNSTFNP 298
QY 301 MYVAFYPMFRKALXMMFLGKIFQKDSRSKCLPL 334
DB 299 MYVAFYPMFRKALXMMFLGKIFQKDSRSKCLPL 332

RESULT 12

ID ABB80695

XX ABB80695 standard; protein; 332 AA.

XX ABB80695;

XX 15-JUL-2002 (first entry)

XX Rat trace amine receptor.

XX Biogenic receptor; trace amine receptor; synaptic transmission; rat;
XX hyperthermia; blood pressure; migraine; cardiac arrhythmia; seizure;

```

KW coma; diabetes; schizophrenia; hypertension; asthma; drug addiction.
XX Rattus norvegicus.
XX WO200222801-A2.
XX 21-MAR-2002.
XX 12-SEP-2001; 2001WO-US028455.
XX 12-SEP-2000; 2000US-00659519.
XX 09-JUL-2001; 2001US-0303967P.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX PA Bunzow JR, Grandy DK, Sonders M;
XX WI; 2002-371971/40.
XX DR N-PSDB; ABL58317.
XX A novel mammalian biogenic amine receptor, useful in assays to identify
XX therapeutic agents for treating e.g., asthma and shock.
XX Claim 5; Fig 2; 86pp; English.
XX The invention relates to novel mammalian (human and rat) biogenic amine
XX receptors. The mammalian biogenic receptors can be used to screen for
XX compounds that bind to it, or to screen for compounds that inhibit a
XX mammalian trace amine receptor. The compounds identified by the assay
XX methods can be used to reduce sympathomimetic effects of enhanced trace
XX amine dependent synaptic transmission in mammals so they can be used to
XX treat the peripheral effects of a drug that binds to or affects the
XX binding to trace amine receptors e.g. hyperthermia, rapid heart rate,
XX high blood pressure, migraine, cardiac arrhythmia, seizure, coma and
XX diabetes or to treat pathological conditions associated with elevated
XX levels of trace amines e.g. schizophrenia, depression, hypertension,
XX shock, cardiac arrhythmias, asthma, migraine, psychosis, anaphylactic
XX reactions and iatrogenic conditions. They are also useful for treating
XX drug addiction. The present sequence represents a rat trace amine
XX receptor
XX SQ Sequence 332 AA;

Query Match 77.3%; Score 1393; DB 5; Length 332;
Best Local Similarity 77.5%; Pred. No. 6.2e-152;
Matches 259; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 1 MELCHNSANISHTNRNWSRSDVRASLYSLIILITLVGNLIVIVISISHFKQLHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSTIDR 120
DB 61 LHSMAVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSTIDR 120
QY 121 YVAVCDPLRYKAKMILVTCVMIFISWSVPVAFAGMIFLELNFKGAEIYKHHVCRGG 180
DB 121 YVAVCDPLRYKAKINLALFWMLISWSLPVAVAFAGMIFLELNLKGVLELYRSQVSDLGG 180
QY 181 CSVFFSKISGVLTFTMTSPYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240
DB 181 CFLFFSKVSGVLAFTMTSPYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240
QY 241 SOSKERKAVKTIGVWGVFLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 300
DB 239 POSKETKAAKTIGVWGVFLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 298
QY 301 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 334
DB 299 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 332

RESULT 13

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AAB49234
ID AAB49234 standard; protein; 332 AA.
XX AAB49234;
XX 14-MAR-2001 (first entry)
XX Mouse SNORF33 receptor protein.
XX SNORF33; inflammation; arthritis; neurological disorder; infection;
XX bone disease; respiratory disorder; asthma; cancer; cardiovascular.
XX OS Mus musculus.
XX WO200073449-A1.
XX 07-DEC-2000.
XX 26-MAY-2000; 2000WO-US014654.
XX 28-MAY-1999; 99US-00322257.
XX 06-OCT-1999; 99US-00413433.
XX (SYNA-) SYNAPTIC PHARM CORP.
XX PI Borowsky BE, Ogozalek KL, Jones KA;
XX WI; 2001-025252/03.
XX Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33 receptor
XX which is useful for designing drugs for treating conditions such as a
XX chronic and acute inflammation, arthritis, neurological disorders and
XX microbial infections.
XX Claim 15; Fig 20; 227pp; English.
XX The present invention relates to a mammalian SNORF33 receptor. SNORF33
XX antagonists and agonists are used to treat abnormalities brought about by
XX increased or decreased activity of the mammalian SNORF33 receptor. The
XX receptor is useful as a tool for designing drugs for treating conditions
XX such as a chronic and acute inflammation, arthritis, neurological
XX disorders, microbial infections, bone diseases, respiratory disorders
XX such as asthma, cancers, cardiovascular disorders
XX SQ Sequence 332 AA;

Query Match 75.0%; Score 1351; DB 4; Length 332;
Best Local Similarity 75.4%; Pred. No. 4.5e-147;
Matches 252; Conservative 31; Mismatches 49; Indels 2; Gaps 1;

QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 1 MELCHAITNISHRNSDWSREVQASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSTIDR 120
DB 61 LHSMAVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSTIDR 120
QY 121 YVAVCDPLRYKAKMILVTCVMIFISWSVPVAFAGMIFLELNFKGAEIYKHHVCRGG 180
DB 121 YVAVCDPLRYKAKINISITLWMLISWSLPVAVAFAGMIFLELNLKGVLELYRSQVSDLGG 180
QY 181 CSVFFSKISGVLTFTMTSPYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240
DB 181 CSPFFSKVSGVLAFTMTSPYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240
QY 241 SOSKERKAVKTIGVWGVFLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 300
DB 239 POSKETKAAKTIGVWGVFLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 298
QY 301 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 334
DB 299 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 332

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RESULT 14
AAG80960
ID AAG80960 standard; protein; 238 AA.
AC AAG80960;
XX
XX 28-AUG-2001 (first entry)
XX Human nGPCR56 #1.
XX G protein-coupled receptor; nGPCR; seven transmembrane receptor;
KW signal transduction; schizophrenia; thyroid disorder; renal failure;
KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KW cardiovascular disease; proliferative disorder; hormonal disorder;
KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KW attention deficit-hyperactivity disorder/attention deficit disorder;
KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KW neuroprotective.
XX
OS Homo sapiens.
XX
XX WO200136473-A2.
XX
XX 25-MAY-2001.
XX
XX 16-NOV-2000; 2000WO-US031581.
XX
XX 16-NOV-1999; 99US-0165838P.
XX 17-NOV-1999; 99US-0166071P.
XX 19-NOV-1999; 99US-0166678P.
XX 28-DEC-1999; 99US-0173396P.
XX 22-FEB-2000; 2000US-0184129P.
XX 28-FEB-2000; 2000US-0185421P.
XX 28-FEB-2000; 2000US-0185554P.
XX 02-MAR-2000; 2000US-0186530P.
XX 03-MAR-2000; 2000US-0186811P.
XX 09-MAR-2000; 2000US-0188114P.
XX 17-MAR-2000; 2000US-0190310P.
XX 21-MAR-2000; 2000US-0190800P.
XX 20-APR-2000; 2000US-0198568P.
XX 02-MAY-2000; 2000US-0201190P.
XX 08-MAY-2000; 2000US-0203111P.
XX 25-MAY-2000; 2000US-0207094P.
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Vogeli G, Wood LS, Parodi LA, Hiebach RR, Lind P, Slightom J;
PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
XX
XX WPI; 2001-389826/41.
XX N-PSDB; AAH51000.
XX
XX New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
PT useful for diagnosing and treating e.g. schizophrenia.
XX
XX Claim 37; Page 86; 261pp; English.
XX
XX The present invention relates to novel G protein-coupled receptors
CC (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
CC one such G protein-coupled receptor. GPCRs are also known as seven
CC transmembrane receptors and function in signal transduction. The nGPCRx
CC coding sequences are useful for screening a human to diagnose a disorder
CC affecting the brain or a genetic predisposition, specifically
CC schizophrenia. nGPCRx are useful for identifying compounds useful for
CC treating schizophrenia. Detection of nGPCRx in a sample is useful as a
CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
CC metabolic and cardiovascular diseases, proliferative disorders and
CC hormonal disorders. Modulators of nGPCRx activity have the utility for

CC treating neurological disorders, including schizophrenia, ADHD/ADD
CC (attention deficit-hyperactivity disorder/attention deficit disorder),
CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC migraine and senile dementia. Additional disorders include inflammatory
CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC diseases e.g. inflammatory bowel disease
XX
SQ Sequence 238 AA;
Query Match 67.0%; Score 1207; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.3e-130;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPFCNNINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKQHTPTNWL 60
DB 11 MPFCNNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKQHTPTNWL 70
QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCHWYFGEVFCVKIHTSTDIMLSSASIFHLSFISIDR 120
DB 71 IHSMATVDFLLGCLVMPYSWVSAEHCHWYFGEVFCVKIHTSTDIMLSSASIFHLSFISIDR 130
QY 121 YYAVCDPLRYKAKMNLIVTCVMIFISWSVPAVFAFGMIFELNFKGAEEIYYKHVHCRGG 180
DB 131 YYAVCDPLRYKAKMNLIVTCVMIFISWSVPAVFAFGMIFELNFKGAEEIYYKHVHCRGG 190
QY 181 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIAKEQARLISDANQ 228
DB 191 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIAKEQARLISDANQ 238
RESULT 15
ABG93778
ID ABG93778 standard; protein; 238 AA.
XX
XX AC ABG93778;
XX
XX 26-NOV-2002 (first entry)
XX
XX Human G protein-coupled receptor protein, beGPCR-seq56.
XX Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
KW nGPCR protein coupled receptor; communication; serpentine structure;
KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KW genetic predisposition; brain; immune response; gene therapy;
KW anxiety disorder; depression; bipolar disorder; schizophrenia;
KW Huntington's disease; dyskinesia; manic depression; stroke;
KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KW tranquiliser.
XX
XX Homo sapiens.
XX
XX WO200264789-A1.
XX
XX 22-AUG-2002.
XX
XX 14-FEB-2001; 2001WO-US004641.
XX
XX 14-FEB-2001; 2001WO-US004641.
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Lind P, Parodi LA, Vogeli G, Wood LS;
XX
XX WPI; 2002-674879/72.
XX N-PSDB; ABS70233.
XX
XX New nucleic acids and polypeptides of the nGPCR protein-coupled receptor,
PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
PT Parkinson's disease.
XX
XX Example 1; Page 81; 244pp; English.

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OM protein - protein search, using sw model

Run on: October 8, 2004, 10:18:51 : Search time 18 Seconds
(without alignments)
969.421 Million cell updates/sec

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Perfect score: 1801
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813.5	45.2	343	2	US-08-788-539A-2
2	782	43.4	338	3	US-09-286-805-4
3	743	41.3	348	3	US-09-286-805-2
4	677.5	37.6	337	2	US-08-467-559B-2
5	534	29.7	360	4	US-09-555-313B-4
6	534	29.7	380	4	US-09-555-313B-24
7	534	29.7	388	1	US-08-446-822-8
8	534	29.7	388	5	PCT-US93-12586-8
9	534	29.7	760	4	US-09-555-313B-2
10	534	29.4	387	1	US-07-996-772A-2
11	529	29.4	387	1	US-08-446-822-2
12	529	29.4	387	4	US-09-328-314-2
13	529	29.4	387	5	PCT-US93-12586-2
14	529	29.4	406	4	US-09-328-314-4
15	529	29.4	406	1	US-07-996-772A-4
16	527	29.3	406	1	US-08-446-822-4
17	527	29.3	406	5	PCT-US93-12586-4
18	527	29.3	358	2	US-08-748-485-6
19	486	27.0	358	1	US-07-817-920-5
20	478.5	26.6	376	1	US-08-117-006-5
21	478.5	26.6	376	1	US-08-216-594-5
22	478.5	26.6	376	5	PCT-US93-00149-5
23	478.5	26.6	375	1	US-08-370-542-5
24	477.5	26.5	375	1	US-08-542-351-5
25	477.5	26.5	375	3	US-09-018-351-5
26	477.5	26.5	359	3	US-08-875-540-15
27	474.5	26.3			

28 474.5 26.3 359 4 US-09-473-634-15 Sequence 15, Appl
29 474 26.3 377 2 US-08-461-812-2 Sequence 2, Appl
30 474 26.3 377 3 US-08-157-185-14 Sequence 14, Appl
31 474 26.3 377 3 US-08-281-526B-14 Sequence 14, Appl
32 474 26.3 377 4 US-09-450-790A-14 Sequence 14, Appl
33 474 26.3 377 4 US-09-332-837-14 Sequence 14, Appl
34 474 26.3 377 4 US-09-371-705-2 Sequence 2, Appl
35 472.5 26.2 359 2 US-08-467-568-13 Sequence 13, Appl
36 472.5 26.2 359 2 US-08-748-485-4 Sequence 2, Appl
37 472.5 26.2 359 2 US-08-103-170-2 Sequence 13, Appl
38 472.5 26.2 359 2 US-09-030-582-13 Sequence 13, Appl
39 472.5 26.2 359 4 US-09-171-456-19 Sequence 19, Appl
40 461.5 25.6 348 3 US-08-875-540-13 Sequence 13, Appl
41 461.5 25.6 348 4 US-09-171-456-17 Sequence 17, Appl
42 461.5 25.6 348 4 US-09-473-634-13 Sequence 13, Appl
43 459.5 25.5 359 2 US-08-748-485-5 Sequence 5, Appl
44 458 25.4 446 1 US-07-626-618A-21 Sequence 21, Appl
45 458 25.4 446 1 US-08-333-977-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-788-539A-2
; Sequence 2, Application US/08788539A
; Patent No. 5871967
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: CLONING OF A NOVEL G-PROTEIN
; TITLE OF INVENTION: COUPLED 7TM RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788.539A
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATGS0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-788-539A-2

Query Match 45.2%; Score 813.5; DB 2; Length 343;
Best Local Similarity 46.0%; Pred. No. 7.3e-64;
Matches 159; Conservative 57; Mismatches 99; Indels 31; Gaps 5;

QY 4 CHNIIN-----ISCVKN-----WSNDVRASLYSLMWLLIITLVLGNLIVIVSIH 49

Db 13 CPKFNKILSSHQPIFSCPGDNVFGDWSHDY-----PFGNLIWVISH 58
QY 50 FQKLTPTNWLHSMATVDFLLGCLVMPYSWVRSAEHCWYFGEVCKIHTSTDMSSAS 109
Db 59 FQKLSPTNWLHSMATVDFLLGCLVMPYSWVRSAEHCWYFGEVCKIHTSTDMSSAS 118
QY 110 IFHLSFISIDRYAVCDPLRYKAKMNLVLCWIFISWVPAVAFGMIFLELNPAGAE 169
Db 119 IFHLSFISIDRYAVCDPLRYKAKMNLVLCWIFISWVPAVAFGMIFLELNPAGAE 178
QY 170 IYKHVHCRGCGSVFPGSKISGVLTFMTSPYIPGSMVLCVYIYIYIAKEOARLISDANOK 229
Db 179 -YKILVACENFALFENKFWGILFTTCFTTGSINWYIGKIFVUSKOHARVISHPEN 237
QY 230 LQIGLEKMGISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPLHYIIPPTNDVLI 289
Db 238 TKGA--VKHLSKKDKAKAATLGIWGVFLACWLPCLFLAVLIDPVDYSTPILIDLIV 295
QY 290 WFGYLNSTNPMVYAFYFWRKALWMLFGKIFQKDSRCKLFE 335
Db 296 WURYFNSTCNPLHGFNFWQAFKFIYVSGKIFSHSETANLFE 341

RESULT 2

US-09-286-805-4
; Sequence 4, Application US/09286805
; Patent No. 6117990
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; TITLE OF INVENTION: DNA Encoding Orphan SNORF1 Receptor
; FILE REFERENCE: 58987
; CURRENT APPLICATION NUMBER: US/09/286,805
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-286-805-4
Query Match 43.4%; Score 782; DB 3; Length 338;
Best Local Similarity 45.8%; Pred. No. 4.2e-61;
Matches 154; Conservative 63; Mismatches 115; Indels 4; Gaps 4;

QY 1 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 60
Db 1 MELCENVNGSCIKSSYSPWRAILYAVLGLGALLAVFGNLLVITAILHFKQLHTPTN 60
QY 61 IHSMTVDLLGCLVMPYSWVRSAEHCWYFGEVCKIHTSTDMSSASIFHLSFISIDR 120
Db 61 VASLACADPLVGTVMFPSTVRSVEGCVFGDTCFDTSCFASFLHLCISIDR 120
QY 121 YVAVCDPLRYKAKMNLVLCWIFISWVPAVAFGMIFLELNPAGAEIYKHVHCRG 180
Db 121 YVAVCDPLRYKAKMNLVLCWIFISWVPAVAFGMIFLELNPAGAEIYKHVHCRG 179
QY 181 CSVFFSKISGVLTFMTSPYIPGSMVLCVYIYIYIAKEOARLISDANOKLQIGLEKMG 239
Db 180 CQAPLNQNVLLCFLL-FELPTVMVFLYGRIFLVAQKQARKIEGSANQPQASSEYKER 238
QY 240 ISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPLHYIIPPTNDVLIWFLYLNSTN 299
Db 239 VAR-RERKAAKTGLIAMAFLVSWLPYIIDAVIDAYMNFITPAYVYVYELLVWCYVYNSAMN 297
QY 300 PMVYAFYFWRKALWMLFGKIFQKDSRCKLFE 335
Db 298 FLIYAFYFWRKALWMLFGKIFQKDSRCKLFE 333

RESULT 3

US-09-286-805-2
; Sequence 2, Application US/09286805
; Patent No. 6117990
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; TITLE OF INVENTION: DNA Encoding Orphan SNORF1 Receptor
; FILE REFERENCE: 58987
; CURRENT APPLICATION NUMBER: US/09/286,805
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-286-805-2
Query Match 41.3%; Score 743; DB 3; Length 348;
Best Local Similarity 42.5%; Pred. No. 1.2e-57;
Matches 141; Conservative 63; Mismatches 126; Indels 2; Gaps 2;

QY 4 CHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWLH 63
Db 14 CYKNVNESCIKTPYSPGPRSIYAVLGFAGVLAAGNLLVMIALLHFKQLHTPTNFI 73
QY 64 MATVDPLGCLVMPYSWVRSAEHCWYFGEVCKIHTSTDMSSASIFHLSFISIDRYA 123
Db 74 LACADPLVGTVMFPSTVRSVEGCVFGDTCFDTSCFASFLHLCISIDRYA 133
QY 124 VCDPLRYKAKMNLVLCWIFISWVPAVAFGMIFLELNPAGAEIYKHVHCRGCGSV 183
Db 134 VTDPLTYPTKFTIVSGVCLSWFVSYSIFVTGANEEGIELVVA-LTCVGGCOA 192
QY 184 FFSKISGVLTFMTSPYIPGSMVLCVYIYIYIAKEOARLISDANOKLQIGLEKMGIS 243
Db 193 PLNQNVLLCFLL-FEIPNVAMVFIYKIFLVAQKQARKIESTASQAQSSSESYKERVAK 251
QY 244 KERKAVKTLGIVMGVFLICWCPFFICTVMDPLHYIIPPTNDVLIWFLYLNSTNPM 303
Db 252 RERKAAKTGLIAMAFLVSWLPYIIDAVIDAYMNFITPAYVYVYELLVWCYVYNSAMN 311
QY 304 AFFYFWRKALWMLFGKIFQKDSRCKLFE 335
Db 312 AFFYFWRKALWMLFGKIFQKDSRCKLFE 343

RESULT 4
US-08-467-559B-2
; Sequence 2, Application US/08467559B
; Patent No. 5928890
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: HUMAN AMINE RECEPTOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,559B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K


```
;
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; FILE REFERENCE: 42667-A-PCT-US
; CURRENT FILING DATE: 1998-04-03
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/446,822
; FILING DATE: June 1, 1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPW/MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-822-8

Query Match      29.7%; Score 534; DB 1; Length 388;
Best Local Similarity 37.4%; Pred. No. 3e-39;
Matches 116; Conservative 53; Mismatches 121; Indels 20; Gaps 5;

QY      25  LYSMLVLIITLVGNLIVIVSIFHKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVR 83
Db      22  LITFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNVIVSLAFADLLVSVLWPFCAIEL 81
QY      84  AEHCWYFGEVFCIKHTSDIMLSSASIPHLISIDRYAV-CDPLRYKAKNMLVICVM 142
Db      82  VQDIWIYGEVFCVLRVTSLDVLLTASIPHLCCISLDRYAICQPLVYRNKMTPLRIALM 141
QY      143  IFISWSVPAVAFAGMIFLELNFKGAEIYYKHVHCRGG---CSVFFSKISGVLTFMTSF 198
Db      142  LGGCWVPTTFISFLPIMQGNWNIIGIDLIEKKFNQNSNTYCVFVWVKNPYAITCSVAF 201
QY      199  YIPGSIMLCVYRIYLIKAEQARLISDANKLQIGLEMKNGISQS-----KERKA 248
Db      202  YIPFLMLVLYRIYVTAKEHAQI-----QMLQAGASSESPQADQHSRMTETKA 257
QY      249  VKTGLVGMVFLICWCPFFICVMDPFLHYIIPPTLNDVLIWFGYLNSTFNMVYAFFYP 308
Db      258  AKTLCIIMGCFCCLWAPFFVTNIVDPFDIYVPGQWTAFLWGLYINSGLNPLFYAFLNK 317
QY      309  WFRKALKMML 318
Db      318  SPRAFLIIL 327

;
; RESULT 8
; US-09-328-314-8
; Sequence 8, Application US/09328314
; Patent No. 6331401
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Brancheck, Theresa
; APPLICANT: Weinsbank, Richard L.
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; FILING DATE:
; CLASSIFICATION:
; APPLICATION NUMBER: PCT/US93/12586
; CURRENT APPLICATION DATA:
; SOFTWARE: Patent In Release #1.24
; OPERATING SYSTEM: PC-DOS/MS-DOS
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; ZIP: 10112
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ADDRESS: COOPER & DUNHAM
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 15
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; GENERAL INFORMATION:
; Sequence 8, Application PC/TUS9312586
; PCT-US93-12586-8
; RESULT 9
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;
; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
; FILE REFERENCE: 42667-AZ-PCT-US
; CURRENT APPLICATION NUMBER: US/09/328,314
; CURRENT FILING DATE: 1998-04-03
; EARLIER FILING DATE: 1995-07-31
; EARLIER FILING DATE: 1995-07-31
; EARLIER FILING DATE: 1995-07-31
; EARLIER FILING DATE: 1993-12-22
; EARLIER FILING DATE: 1993-12-22
; EARLIER FILING DATE: 1992-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-328-314-8

Query Match      29.7%; Score 534; DB 4; Length 388;
Best Local Similarity 37.4%; Pred. No. 3e-39;
Matches 116; Conservative 53; Mismatches 121; Indels 20; Gaps 5;

QY      25  LYSMLVLIITLVGNLIVIVSIFHKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVR 83
Db      22  LITFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNVIVSLAFADLLVSVLWPFCAIEL 81
QY      84  AEHCWYFGEVFCIKHTSDIMLSSASIPHLISIDRYAV-CDPLRYKAKNMLVICVM 142
Db      82  VQDIWIYGEVFCVLRVTSLDVLLTASIPHLCCISLDRYAICQPLVYRNKMTPLRIALM 141
QY      143  IFISWSVPAVAFAGMIFLELNFKGAEIYYKHVHCRGG---CSVFFSKISGVLTFMTSF 198
Db      142  LGGCWVPTTFISFLPIMQGNWNIIGIDLIEKKFNQNSNTYCVFVWVKNPYAITCSVAF 201
QY      199  YIPGSIMLCVYRIYLIKAEQARLISDANKLQIGLEMKNGISQS-----KERKA 248
Db      202  YIPFLMLVLYRIYVTAKEHAQI-----QMLQAGASSESPQADQHSRMTETKA 257
QY      249  VKTGLVGMVFLICWCPFFICVMDPFLHYIIPPTLNDVLIWFGYLNSTFNMVYAFFYP 308
Db      258  AKTLCIIMGCFCCLWAPFFVTNIVDPFDIYVPGQWTAFLWGLYINSGLNPLFYAFLNK 317
QY      309  WFRKALKMML 318
Db      318  SPRAFLIIL 327

;
; RESULT 9
; PCT-US93-12586-8
; Sequence 8, Application PC/TUS9312586
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12586
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
```

; REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-12586-8

Query Match 29.7%; Score 534; DB 5; Length 388;
Best Local Similarity 37.4%; Pred. No. 3e-39;
Matches 116; Conservative 53; Mismatches 121; Indels 20; Gaps 5;

QY 25 LYSMLVLIITLVGNLIVIVISISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVRS 83
DB 22 LTFSTVILMAILGNLLVMVAVCDRLRKTKNYFIVSLAFADLLVSLVMPFGAIEL 81
QY 84 AEHCWYFGEVCKIHTSTDIMLSSASIFHLSFISIDRYAV-CDPLRYKAKNIIIVICM 142
DB 82 VQDIWYGEVCLVTSLDVLLTTASIFHLCCISLDRYVAICQPLVYRNKMTPLRIALM 141
QY 143 IFISWSVPAVAFGMIFLELNFKGAEIYYKHVHCRGG-----CSVFFSKISGLVTFMTSF 198
DB 142 LGGCWVIPTFISFLPMQGNNGIIDLIERKFNQNSNSTYCVPMVANKPYAITCSVAVF 201
QY 199 YIPGSIMLCVYRYIYLIKAEQARLISDANQKLIQIGLEMKNGISQS-----KERKA 248
DB 202 YIPFLMLVAYRIYVTAKEHAHQI-----QMLQAGASESRPQADQHSHTRMETETKA 257
QY 249 VKTLGIVMGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNMVYAFYFP 308
DB 258 AKTLCIINGCFCCLWAPFFVNIIVDPFDIDYTPGQVWTAFLWGLYNSGLNPLFYAFLNK 317
QY 309 WFRKALKMML 318
DB 318 SFRRFLIIL 327

RESULT 10
US-09-555-313B-2
; Sequence 2, Application US/09555313B
; Patent No. 6506590
; GENERAL INFORMATION:
; APPLICANT: FICHSMEISTER, Rudolph et al.
; TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
; TITLE OF INVENTION: 5-HT4 and uses thereof, in particular for screening
; FILE REFERENCE: P06762US00/BAS
; CURRENT APPLICATION NUMBER: US/09/555,313B
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: FR 97/15037
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-555-313B-2

Query Match 29.7%; Score 534; DB 4; Length 760;
Best Local Similarity 37.4%; Pred. No. 6.4e-39;
Matches 116; Conservative 53; Mismatches 121; Indels 20; Gaps 5;

QY 25 LYSMLVLIITLVGNLIVIVISISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVRS 83
DB 22 LTFSTVILMAILGNLLVMVAVCDRLRKTKNYFIVSLAFADLLVSLVMPFGAIEL 81
QY 84 AEHCWYFGEVCKIHTSTDIMLSSASIFHLSFISIDRYAV-CDPLRYKAKNIIIVICM 142

DB 82 VQDIWYGEVCLVTSLDVLLTTASIFHLCCISLDRYVAICQPLVYRNKMTPLRIALM 141
QY 143 IFISWSVPAVAFGMIFLELNFKGAEIYYKHVHCRGG-----CSVFFSKISGLVTFMTSF 198
DB 142 LGGCWVIPTFISFLPMQGNNGIIDLIERKFNQNSNSTYCVPMVANKPYAITCSVAVF 201
QY 199 YIPGSIMLCVYRYIYLIKAEQARLISDANQKLIQIGLEMKNGISQS-----KERKA 248
DB 202 YIPFLMLVAYRIYVTAKEHAHQI-----QMLQAGASESRPQADQHSHTRMETETKA 257
QY 249 VKTLGIVMGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNMVYAFYFP 308
DB 258 AKTLCIINGCFCCLWAPFFVNIIVDPFDIDYTPGQVWTAFLWGLYNSGLNPLFYAFLNK 317
QY 309 WFRKALKMML 318
DB 318 SFRRFLIIL 327

RESULT 11
US-07-996-772A-2
; Sequence 2, Application US/07996772A
; Patent No. 5472866
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branche, Theresa A.
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/996,772A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-996-772A-2

Query Match 29.4%; Score 529; DB 1; Length 387;
Best Local Similarity 35.4%; Pred. No. 8.3e-39;
Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

QY 25 LYSMLVLIITLVGNLIVIVISISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVRS 83
DB 22 LTFAMVILMAILGNLLVMVAVCDRLRKTKNYFIVSLAFADLLVSLVMPFGAIEL 81
QY 84 AEHCWYFGEVCKIHTSTDIMLSSASIFHLSFISIDRYAV-CDPLRYKAKNIIIVICM 142
DB 82 VQDIWYGEVCLVTSLDVLLTTASIFHLCCISLDRYVAICQPLVYRNKMTPLRIALM 141

QY 143 IFISWSVAVFAPGMIFFLELNFKAEEIY----YKHVHCRGCSVFFFSKISGVLFTMTSF 198
 Db 142 LGGCWVPMFISFLPMQWNNIGIVDVIEKKFNHNSNSTFCVFMVKNPVAITCSVAVF 201
 QY 199 YIPGSIMLCVYRYIYLIAKEOARLISDANKLOIGLEMKNGISQSK-----244
 Db 202 YIPFLLMVLAYRYIVTAKAHEA-----QQIQM-LQRAGATSESRPQADQSHTRMRT 253
 QY 245 ERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFPMVYA 304
 Db 254 ETAKAATLCVINGCFCFCWAPFFVTNIVDPFDITYVPEKVTAFWLWGLVINGSLNPLFYA 313
 QY 305 FFPWFRKALKOML 318
 Db 314 FLNKSFRRAFLIIL 327

RESULT 12
 US-08-446-822-2
 ; Sequence 2, Application US/08446822
 ; Patent No. 5766879
 ; GENERAL INFORMATION:
 ; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
 ; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: COOPER & DUNHAM
 ; STREET: 30 ROCKEFELLER PLAZA
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,822
 ; FILING DATE: June 1, 1995
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, P. John
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPW/WAT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0525
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 387 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-446-822-2

Query Match 29.4%; Score 529; DB 1; Length 387;
 Best Local Similarity 35.4%; Pred. No. 8.3e-39;
 Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;
 QY 25 LYSMLVLIITLVGNLIVIVSISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSWVRS 83
 Db 22 LLTPFAMVILMAILGNLLVMVAVCDRLQRKIKTYFIVSLAFADLLVSLVNAFGATEL 81
 QY 84 AEHCWYFGEVFCIKHTSDIMLSSASIFHLGFSISIDRYAV-CDPLRYKAKNNILVICW 142
 Db 82 VQDIWFYGEMLCVRTSLDVLTTASIFHLCCISLDRYAICCCQPLVYRNKMTPLRIALM 141
 QY 143 IFISWSVAVFAPGMIFFLELNFKAEEIY----YKHVHCRGCSVFFFSKISGVLFTMTSF 198
 Db 142 LGGCWVPMFISFLPMQWNNIGIVDVIEKKFNHNSNSTFCVFMVKNPVAITCSVAVF 201

QY 199 YIPGSIMLCVYRYIYLIAKEOARLISDANKLOIGLEMKNGISQSK-----244
 Db 202 YIPFLLMVLAYRYIVTAKAHEA-----QQIQM-LQRAGATSESRPQADQSHTRMRT 253
 QY 245 ERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFPMVYA 304
 Db 254 ETAKAATLCVINGCFCFCWAPFFVTNIVDPFDITYVPEKVTAFWLWGLVINGSLNPLFYA 313
 QY 305 FFPWFRKALKOML 318
 Db 314 FLNKSFRRAFLIIL 327

RESULT 13
 US-09-328-314-2
 ; Sequence 2, Application US/09328314
 ; Patent No. 6331401
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartig, Christophe
 ; APPLICANT: Branchek, Theresa
 ; APPLICANT: Weinshank, Richard L.
 ; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
 ; FILE REFERENCE: 42667-AZ-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/328,314
 ; EARLIER FILING DATE: 1998-04-03
 ; EARLIER APPLICATION NUMBER: 08/446,822
 ; EARLIER FILING DATE: 1995-07-31
 ; EARLIER APPLICATION NUMBER: PCT/US93/12586
 ; EARLIER FILING DATE: 1993-12-22
 ; EARLIER APPLICATION NUMBER: 07/996,772
 ; EARLIER FILING DATE: 1992-12-24
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 387
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-328-314-2

Query Match 29.4%; Score 529; DB 4; Length 387;
 Best Local Similarity 35.4%; Pred. No. 8.3e-39;
 Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;
 QY 25 LYSMLVLIITLVGNLIVIVSISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSWVRS 83
 Db 22 LLTPFAMVILMAILGNLLVMVAVCDRLQRKIKTYFIVSLAFADLLVSLVNAFGATEL 81
 QY 84 AEHCWYFGEVFCIKHTSDIMLSSASIFHLGFSISIDRYAV-CDPLRYKAKNNILVICW 142
 Db 82 VQDIWFYGEMLCVRTSLDVLTTASIFHLCCISLDRYAICCCQPLVYRNKMTPLRIALM 141
 QY 143 IFISWSVAVFAPGMIFFLELNFKAEEIY----YKHVHCRGCSVFFFSKISGVLFTMTSF 198
 Db 142 LGGCWVPMFISFLPMQWNNIGIVDVIEKKFNHNSNSTFCVFMVKNPVAITCSVAVF 201
 QY 199 YIPGSIMLCVYRYIYLIAKEOARLISDANKLOIGLEMKNGISQSK-----244
 Db 202 YIPFLLMVLAYRYIVTAKAHEA-----QQIQM-LQRAGATSESRPQADQSHTRMRT 253
 QY 245 ERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFPMVYA 304
 Db 254 ETAKAATLCVINGCFCFCWAPFFVTNIVDPFDITYVPEKVTAFWLWGLVINGSLNPLFYA 313
 QY 305 FFPWFRKALKOML 318
 Db 314 FLNKSFRRAFLIIL 327

RESULT 14
 PCT-US93-12586-2
 ; Sequence 2, Application PC/TUS9312586
 ; GENERAL INFORMATION:

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; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12586
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-12586-2

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Query Match      29.4%; Score 529; DB 5; Length 387;
Best Local Similarity 35.4%; Pred. No. 8.3e-39;
Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

QY 25 LYSMLVLILTLVGNLIVIVISISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVRS 83
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 LITFPAMVILMAILGNLLVMVAVCDRQLRKTKTYFIVSLAFADLLVSLVNAFGAIEL 81
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 84 AEHCWYFGEVFCCKHTSTDMILSSASIFHLISIDRYAV-CDPLRYKAKNNILVICVM 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 VQDIWFYGEMLCVRTSLDVLTTASIFHLCCISLDRYAICCPPLVYRNKMTPLRIALM 141
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 143 IFISWSVPAVFAFGMIFLELNFKAEEIY----YKHVHCRGCGSVFFSKISGLVTFMTSF 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 LGGCWVIFMFISFLPMQGNNGIVDVIEKRKFHNNSNFTCFVFNKPYAITCSVAVF 201
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 199 YIPGSIMLCVYRIYLIKAQEARLISDANQKIQIGLEMKNGISQSK----- 244
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 YIPFLMWLAYRIYVTTAKEHA-----QQIQM-LORAGATSESRPQTADQHSRMRWT 253
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 245 ERKAVKTLGIWVGVLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTENPMVYA 304
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 254 ETKAAKTLGVIMGCFPCWAPFFVTNIVDPFDITVPEKVTAFPLWGLVYNSGLNPFLEYA 313
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 305 FFYPWFRKALKMML 318
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 314 FLNKSFRRAFLIIL 327
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

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RESULT 15
US-09-328-314-4
; Sequence 4, Application US/09328314
; Patent No. 6331401
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Brancheck, Theresa
; APPLICANT: Weinshank, Richard L.

```

```

; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
; FILE REFERENCE: 42667-AZ-PCT-US
; CURRENT APPLICATION NUMBER: US/09/328,314
; CURRENT FILING DATE: 1998-04-03
; EARLIER APPLICATION NUMBER: 08/446,822
; EARLIER FILING DATE: 1995-07-31
; EARLIER APPLICATION NUMBER: PCT/US93/12586
; EARLIER FILING DATE: 1993-12-22
; EARLIER APPLICATION NUMBER: 07/996,772
; EARLIER FILING DATE: 1992-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-328-314-4

```

```

Query Match      29.4%; Score 529; DB 4; Length 406;
Best Local Similarity 35.4%; Pred. No. 8.7e-39;
Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

QY 25 LYSMLVLILTLVGNLIVIVISISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVRS 83
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 LITFPAMVILMAILGNLLVMVAVCDRQLRKTKTYFIVSLAFADLLVSLVNAFGAIEL 81
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 84 AEHCWYFGEVFCCKHTSTDMILSSASIFHLISIDRYAV-CDPLRYKAKNNILVICVM 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 VQDIWFYGEMLCVRTSLDVLTTASIFHLCCISLDRYAICCPPLVYRNKMTPLRIALM 141
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 143 IFISWSVPAVFAFGMIFLELNFKAEEIY----YKHVHCRGCGSVFFSKISGLVTFMTSF 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 LGGCWVIFMFISFLPMQGNNGIVDVIEKRKFHNNSNFTCFVFNKPYAITCSVAVF 201
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 199 YIPGSIMLCVYRIYLIKAQEARLISDANQKIQIGLEMKNGISQSK----- 244
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 YIPFLMWLAYRIYVTTAKEHA-----QQIQM-LORAGATSESRPQTADQHSRMRWT 253
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 245 ERKAVKTLGIWVGVLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTENPMVYA 304
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 254 ETKAAKTLGVIMGCFPCWAPFFVTNIVDPFDITVPEKVTAFPLWGLVYNSGLNPFLEYA 313
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 305 FFYPWFRKALKMML 318
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 314 FLNKSFRRAFLIIL 327
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Job time : 20 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2004, 10:20:11 : Search time 130 Seconds
(without alignments)
836.678 Million cell updates/sec

Title: US-09-633-145-2

Perfect score: 1801

Sequence: 1 MPFCHNIINISVKWNWSD.....FGKIFQKDSRCKLFLELSS 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/ECTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1801	100.0	339	9	US-09-995-225-12
2	1801	100.0	339	10	US-09-782-974C-90
3	1801	100.0	339	10	US-09-995-225-12
4	1801	100.0	339	14	US-10-267-217-6
5	1801	100.0	339	14	US-10-225-567A-639
6	1801	100.0	339	15	US-10-085-198-190
7	1801	100.0	339	15	US-10-085-198-192
8	1801	100.0	339	15	US-10-085-198-200
9	1786	99.2	339	12	US-10-380-614-2
10	1786	99.2	339	16	US-10-769-131-2
11	1520	84.4	296	10	US-09-782-974C-88
12	1403	77.9	332	14	US-10-267-217-4
13	1393	77.3	332	12	US-10-380-614-4
14	1393	77.3	332	16	US-10-769-131-4
15	1207	67.0	238	10	US-09-782-974C-64

15	998	55.4	191	14	US-10-267-217-2	Sequence 2, Appli
17	848	47.1	351	9	US-09-474-696-2	Sequence 2, Appli
18	848	47.1	351	14	US-10-307-736-2	Sequence 2, Appli
19	815	45.3	306	14	US-10-225-567A-577	Sequence 577, App
20	813.5	45.2	343	9	US-09-742-869-2	Sequence 2, Appli
21	813.5	45.2	343	14	US-10-225-567A-579	Sequence 579, App
22	805.5	44.7	296	14	US-10-251-852-6	Sequence 6, Appli
23	743	41.3	348	14	US-10-225-567A-645	Sequence 645, App
24	718	39.9	345	14	US-10-230-007B-2	Sequence 2, Appli
25	718	39.9	345	16	US-10-647-982A-2	Sequence 2, Appli
26	715	39.7	345	9	US-09-995-225-10	Sequence 10, Appli
27	715	39.7	345	10	US-09-782-974C-84	Sequence 84, Appli
28	715	39.7	345	10	US-09-995-225-10	Sequence 10, Appli
29	715	39.7	345	14	US-10-225-567A-685	Sequence 685, App
30	715	39.7	345	14	US-10-251-852-2	Sequence 2, Appli
31	715	39.7	345	15	US-10-085-198-196	Sequence 196, App
32	696	38.6	342	9	US-09-995-225-14	Sequence 14, Appli
33	696	38.6	342	10	US-09-791-932-118	Sequence 118, App
34	696	38.6	342	10	US-09-995-225-14	Sequence 14, Appli
35	696	38.6	342	14	US-10-225-567A-687	Sequence 687, App
36	696	38.6	342	15	US-10-232-798-998	Sequence 998, App
37	696	38.6	342	15	US-10-085-198-194	Sequence 194, App
38	694	38.5	342	14	US-10-330-220-2	Sequence 2, Appli
39	677.5	37.6	337	12	US-09-988-745-2	Sequence 2, Appli
40	677.5	37.6	337	14	US-10-180-946-2	Sequence 2, Appli
41	677.5	37.6	337	14	US-10-225-567A-358	Sequence 358, App
42	677.5	37.6	337	16	US-10-408-765A-482	Sequence 482, App
43	675	37.5	332	16	US-10-398-036-9	Sequence 9, Appli
44	671.5	37.3	321	14	US-10-330-220-4	Sequence 4, Appli
45	671.5	37.3	321	14	US-10-251-852-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-995-225-12
; Sequence 12, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208

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; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-12

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Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 IHSMATVDFLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 120
Db 62 IHSMATVDFLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 121
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Db 122 YVAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFLELNFKAEEIYYKHVHCRCG 181
QY 181 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYIRYLYIAKEQARLISDANKQLQIGLEMKNGI 240
Db 182 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYIRYLYIAKEQARLISDANKQLQIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
Db 242 SOSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
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Db 302 MYVAFYFPWFRKALKXMLFGKIFQKDSRCKLFLELSS 339

RESULT 2
US-09-782-974C-90
; Sequence 90, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 41USPRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
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; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-90

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Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 182 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYIRYLYIAKEQARLISDANKQLQIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
Db 242 SOSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
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Db 302 MYVAFYFPWFRKALKXMLFGKIFQKDSRCKLFLELSS 339

RESULT 3
US-09-995-225-12
; Sequence 12, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
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; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-12

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Best Local Similarity 100.0%; Pred. No. 3.2e-156;
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DB 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
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RESULT 4
US-10-267-217-6
; Sequence 6, Application US/10267217
; Publication No. US20030105318A1
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Gogozalek, Kristine L.
; APPLICANT: Jones, Kenneth A.
; TITLE OF INVENTION: DNA Encoding SNORF33 Receptor
; FILE REFERENCE: 59338A
; CURRENT APPLICATION NUMBER: US/10/267,217
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/09/413,433
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 09/322,257
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 6
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-217-6

Query Match 100.0%; Score 1801; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 62 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 180
DB 122 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 181
QY 181 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQARLISDANQKIQIGLEMKNGI 240
DB 182 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQARLISDANQKIQIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
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QY 301 MYAFFYFWRKALKMFLFGKIFQKDSRCKLFLELSS 338
DB 302 MYAFFYFWRKALKMFLFGKIFQKDSRCKLFLELSS 339

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DB 62 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 180
DB 122 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 181
QY 181 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQARLISDANQKIQIGLEMKNGI 240
DB 182 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQARLISDANQKIQIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
QY 301 MYAFFYFWRKALKMFLFGKIFQKDSRCKLFLELSS 338
DB 302 MYAFFYFWRKALKMFLFGKIFQKDSRCKLFLELSS 339

RESULT 5

US-10-225-567A-639
; Sequence 639, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 639
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-639

Query Match 100.0%; Score 1801; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 62 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 180
DB 122 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 181
QY 181 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQARLISDANQKIQIGLEMKNGI 240
DB 182 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQARLISDANQKIQIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
QY 301 MYAFFYFWRKALKMFLFGKIFQKDSRCKLFLELSS 338
DB 302 MYAFFYFWRKALKMFLFGKIFQKDSRCKLFLELSS 339

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RESULT 6
US-10-085-198-190
; Sequence 190, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-25
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-08-13
; PRIOR FILING DATE: 2001-08-16
; PRIOR FILING DATE: 2001-08-27
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2001-03-27
; PRIOR FILING DATE: 2001-04-21
; PRIOR FILING DATE: 2001-06-20
; PRIOR FILING DATE: 2001-08-29
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 190
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-190

Query Match      100.0%; Score 1801; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61

QY 61 IHSMATVDPLGLCLWMPYSWVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 120
DB 62 IHSMATVDPLGLCLWMPYSWVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 121

QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 180
DB 122 YVAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 181

QY 181 CSVFSKISGVLTFMTSFYIPGSIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 240
DB 182 CSVFSKISGVLTFMTSFYIPGSIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 241

QY 241 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301

QY 301 MYAIFYPWFRRKALKOMLFGKIFQKDSRRCKLFLFLSS 338
DB 302 MYAIFYPWFRRKALKOMLFGKIFQKDSRRCKLFLFLSS 339

RESULT 7
US-10-085-198-192
; Sequence 192, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-25
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-08-13
; PRIOR FILING DATE: 2001-08-16
; PRIOR FILING DATE: 2001-08-27
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; PRIOR FILING DATE: 2001-03-27
; PRIOR FILING DATE: 2001-04-21
; PRIOR FILING DATE: 2001-06-20
; PRIOR FILING DATE: 2001-08-29
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 190
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-192

Query Match      100.0%; Score 1801; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61

QY 61 IHSMATVDPLGLCLWMPYSWVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 120
DB 62 IHSMATVDPLGLCLWMPYSWVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 121

QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 180
DB 122 YVAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 181

QY 181 CSVFSKISGVLTFMTSFYIPGSIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 240
DB 182 CSVFSKISGVLTFMTSFYIPGSIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 241

QY 241 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301

QY 301 MYAIFYPWFRRKALKOMLFGKIFQKDSRRCKLFLFLSS 338
DB 302 MYAIFYPWFRRKALKOMLFGKIFQKDSRRCKLFLFLSS 339
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Publication No. US20040009907A1
GENERAL INFORMATION:
APPLICANT: Alsobrook et al.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-279
CURRENT APPLICATION NUMBER: 60/271,646
PRIOR FILING DATE: 2001-02-25
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-27
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-04-21
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-02-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 653
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 192
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-10-085-198-192

Query Match      100.0%; Score 1801; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61

QY 61 IHSMATVDPLGLCLWMPYSWVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 120
DB 62 IHSMATVDPLGLCLWMPYSWVRSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 121

QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 180
DB 122 YVAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 181

QY 181 CSVFSKISGVLTFMTSFYIPGSIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 240
DB 182 CSVFSKISGVLTFMTSFYIPGSIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 241

QY 241 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301

QY 301 MYAIFYPWFRRKALKOMLFGKIFQKDSRRCKLFLFLSS 338
DB 302 MYAIFYPWFRRKALKOMLFGKIFQKDSRRCKLFLFLSS 339

RESULT 8
US-10-085-198-200
; Sequence 200, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
```

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; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 200
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-200

Query Match
Best Local Similarity 100.0%; Score 1801; DB 15; Length 339;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFQKQHTPTNWL 60
Db 2 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFQKQHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTIDMLSSAIFHLSPFISIDR 120
Db 62 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTIDMLSSAIFHLSPFISIDR 121
QY 121 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKAEEIYKXVHCRCG 180
Db 122 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKAEEIYKXVHCRCG 181
QY 181 CSVFFSKISGVLTFMTSFYIPGSIMLCVYRYLYIAKEQARLISDANQKIQIGLEMKNGI 240
Db 182 CLVFFSKISGVLTFMTSFYIPGSIMLCVYRYLYIAKEQARLISDANQKIQIGLEMKNGI 241
QY 241 SOSKERVAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
Db 242 SOSKERVAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
QY 301 MYAFYFPWFRKALXKMLFGKIFQKDSRCKLFLELSS 338
Db 302 MYAFYFPWFRKALXKMLFGKIFQKDSRCKLFLELSS 339

RESULT 9
US-10-380-614-2
; Sequence 2, Application US/10380614
; Publication No. US20040072187A1
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James
; APPLICANT: Grandy, David
; TITLE OF INVENTION: Novel Mammalian Receptor Genes and Uses
; FILE REFERENCE: 98-520-E
; CURRENT APPLICATION NUMBER: US/10/380,614
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/659,519

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; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: PCT/US01/28455
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/303,967
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-614-2

Query Match
Best Local Similarity 99.2%; Score 1786; DB 12; Length 339;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFQKQHTPTNWL 60
Db 2 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFQKQHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTIDMLSSAIFHLSPFISIDR 120
Db 62 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTIDMLSSAIFHLSPFISIDR 121
QY 121 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKAEEIYKXVHCRCG 180
Db 122 YYAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKAEEIYKXVHCRCG 181
QY 181 CSVFFSKISGVLTFMTSFYIPGSIMLCVYRYLYIAKEQARLISDANQKIQIGLEMKNGI 240
Db 182 CLVFFSKISGVLTFMTSFYIPGSIMLCVYRYLYIAKEQARLISDANQKIQIGLEMKNGI 241
QY 241 SOSKERVAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
Db 242 SOSKERVAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
QY 301 MYAFYFPWFRKALXKMLFGKIFQKDSRCKLFLELSS 338
Db 302 MYAFYFPWFRKALXKMLFGKIFQKDSRCKLFLELSS 339

RESULT 10
US-10-769-131-2
; Sequence 2, Application US/10769131
; Publication No. US20040142390A1
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James
; APPLICANT: Grandy, David
; TITLE OF INVENTION: Novel Mammalian Catecholamine Receptor Genes and Uses
; FILE REFERENCE: 98-520
; CURRENT APPLICATION NUMBER: US/10/769,131
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-769-131-2

Query Match
Best Local Similarity 99.2%; Score 1786; DB 16; Length 339;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFQKQHTPTNWL 60
Db 2 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFQKQHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTIDMLSSAIFHLSPFISIDR 120
Db 62 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTIDMLSSAIFHLSPFISIDR 121

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QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGAEIYYKHVHCRCG 180
 DB 122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGAEIYYKHVHCRCG 181
 QY 181 CSVFFSKISGVLTFMTSFYIPGSMILCVYRIRYLIYLAKEQARLISDANOKLQIGLEMKNGI 240
 DB 182 CLVFFSKISGVLTFMTSFYIPGSMILCVYRIRYLIYLAKEQARLISDANOKLQIGLEMKNGI 241
 QY 241 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 DB 242 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
 QY 301 MYVAFYFPFRKALKMVLFGKIFQKDSRSRCKLFL 338
 DB 302 MYVAFYFPFRKALKMVLFGKIFQKDSRSRCKLFL 339

RESULT 11
 US-09-782-974C-88
 ; Sequence 88, Application US/09782974C
 ; Publication No. US20030082534A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogel, Gabriel
 ; APPLICANT: Lind, Peter
 ; APPLICANT: Wood, Linda S.
 ; APPLICANT: Parodi, Luis A.
 ; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
 ; FILE REFERENCE: 411USPHRM311
 ; CURRENT APPLICATION NUMBER: US/09/782,974C
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 60/165,838
 ; PRIOR FILING DATE: 1999-11-16
 ; PRIOR APPLICATION NUMBER: 09/714,449
 ; PRIOR FILING DATE: 2000-11-16
 ; PRIOR APPLICATION NUMBER: 60/198,568
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: 60/166,071
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 60/166,678
 ; PRIOR FILING DATE: 1999-11-19
 ; PRIOR APPLICATION NUMBER: 60/173,396
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: 60/184,129
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: 60/185,421
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: 60/185,554
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: 60/186,530
 ; PRIOR FILING DATE: 2000-03-02
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 192
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 88
 ; LENGTH: 296
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-974C-88

Query Match 84.4%; Score 1520; DB 10; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.3e-130;
 Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIIVIVISHFQKLTHTPTNWL 60
 DB 2 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIIVIVISHFQKLTHTPTNWL 61
 QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSTFISIDR 120
 DB 62 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSTFISIDR 121
 QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGAEIYYKHVHCRCG 180

DB 122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGAEIYYKHVHCRCG 181
 QY 181 CSVFFSKISGVLTFMTSFYIPGSMILCVYRIRYLIYLAKEQARLISDANOKLQIGLEMKNGI 240
 DB 182 CSVFFSKISGVLTFMTSFYIPGSMILCVYRIRYLIYLAKEQARLISDANOKLQIGLEMKNGI 241
 QY 241 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLND 286
 DB 242 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLND 287

RESULT 12
 US-10-267-217-4
 ; Sequence 4, Application US/10267217
 ; Publication No. US20030105318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borowsky, Beth E.
 ; APPLICANT: Ogozalek, Kristine L.
 ; APPLICANT: Jones, Kenneth A.
 ; TITLE OF INVENTION: DNA Encoding SNORF33 Receptor
 ; FILE REFERENCE: 59338A
 ; CURRENT APPLICATION NUMBER: US/10/267,217
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: US/09/413,433
 ; PRIOR FILING DATE: 1999-10-06
 ; PRIOR APPLICATION NUMBER: 09/322,257
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: Patent in Ver. 2.0 - beta
 ; SEQ ID NO 4
 ; LENGTH: 332
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-267-217-4

Query Match 77.9%; Score 1403; DB 14; Length 332;
 Best Local Similarity 78.1%; Pred. No. 7.3e-120;
 Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;
 QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIIVIVISHFQKLTHTPTNWL 60
 DB 1 MHLCHNSANISHTNSWSDVRASLYSLMVLIIITLVGNLIIVIVISHFQKLTHTPTNWL 60
 QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSTFISIDR 120
 DB 61 LHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSTFISIDR 120
 QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGAEIYYKHVHCRCG 180
 DB 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGAEIYYKHVHCRCG 180
 QY 181 CSVFFSKISGVLTFMTSFYIPGSMILCVYRIRYLIYLAKEQARLISDANOKLQIGLEMKNGI 240
 DB 181 CFPFFSKVSGVLAFMTSFYIPGSMILCVYRIRYLIYLAKEQARLISDANOKLQIGLEMKNGI 238
 QY 241 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 DB 239 PQSKETKAAKTLGIMVGVLFCWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 298
 QY 301 MYVAFYFPFRKALKMVLFGKIFQKDSRSRCKLFL 334
 DB 299 MYVAFYFPFRKALKMVLFGKIFQKDSRSRCKLFL 332

RESULT 13
 US-10-380-614-4
 ; Sequence 4, Application US/10380614
 ; Publication No. US20040072187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oregon Health and Science University
 ; APPLICANT: Bunzow, James
 ; APPLICANT: Grandy, David
 ; TITLE OF INVENTION: Novel Mammalian Receptor Genes and Uses

FILE REFERENCE: 98-520-E
 CURRENT APPLICATION NUMBER: US/10/380,614
 CURRENT FILING DATE: 2003-08-04
 PRIOR APPLICATION NUMBER: US 09/659,519
 PRIOR FILING DATE: 2000-09-12
 PRIOR APPLICATION NUMBER: PCT/US01/28455
 PRIOR FILING DATE: 2001-09-12
 PRIOR APPLICATION NUMBER: US 60/303,967
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patent in version 3.0
 SEQ ID NO 4
 LENGTH: 332
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-10-380-614-4

Query Match 77.3%; Score 1393; DB 12; Length 332;
 Best Local Similarity 77.5%; Pred. No. 6e-119;
 Matches 259; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

QY	1	MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFQKQHTPTNWL	60
DB	1	MELCHNSANISHTNRNWSRDRASLYSLIIITLVGNLIVIVISISHFQKQHTPTNWL	60
QY	61	IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASIFHLFSISDR	120
DB	61	LHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASIFHLFSISDR	120
QY	121	YAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFELNFKGAEIYKHHVCRGG	180
DB	121	YAVCDPLRYKAKINLAIFVMLISWSLPVAFAGMIFELNFKGAEIYKHHVCRGG	180
QY	181	CSVFFSKISGVLTFTMTSFYIPGSMICVYRIYLIKEQARLISDANQKIQIGLEMKNGI	240
DB	181	CSVFFSKISGVLTFTMTSFYIPGSMICVYRIYLIKEQARLISDANQKIQIGLEMKNGI	240
QY	241	SQSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYLNSTFNP	300
DB	241	SQSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYLNSTFNP	300
QY	299	POSKETKAATLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYLNSTFNP	298
DB	299	POSKETKAATLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYLNSTFNP	298
QY	301	MYAFYFPWFRKALXWMLFGKIFQKDSRSCKLFL	334
DB	299	MYAFYFPWFRKALXWMLFGKIFQKDSRSCKLFL	332

RESULT 14
 US-10-769-131-4
 Sequence 4, Application US/10769131
 Publication No. US20040142390A1
 GENERAL INFORMATION:
 APPLICANT: Bunzow, James
 APPLICANT: Grandy, David
 TITLE OF INVENTION: Novel Mammalian Catecholamine Receptor Genes and Uses
 FILE REFERENCE: 98-520
 CURRENT APPLICATION NUMBER: US/10/769,131
 CURRENT FILING DATE: 2004-01-30
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patent in version 3.0
 SEQ ID NO 4
 LENGTH: 332
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-10-769-131-4

Query Match 77.3%; Score 1393; DB 16; Length 332;
 Best Local Similarity 77.5%; Pred. No. 6e-119;
 Matches 259; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

QY	1	MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFQKQHTPTNWL	60
DB	1	MELCHNSANISHTNRNWSRDRASLYSLIIITLVGNLIVIVISISHFQKQHTPTNWL	60

QY	61	IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASIFHLFSISDR	120
DB	61	LHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASIFHLFSISDR	120
QY	121	YAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFELNFKGAEIYKHHVCRGG	180
DB	121	YAVCDPLRYKAKINLAIFVMLISWSLPVAFAGMIFELNFKGAEIYKHHVCRGG	180
QY	181	CSVFFSKISGVLTFTMTSFYIPGSMICVYRIYLIKEQARLISDANQKIQIGLEMKNGI	240
DB	181	CSVFFSKISGVLTFTMTSFYIPGSMICVYRIYLIKEQARLISDANQKIQIGLEMKNGI	240
QY	241	SQSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYLNSTFNP	300
DB	241	SQSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYLNSTFNP	300
QY	299	POSKETKAATLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYLNSTFNP	298
DB	299	POSKETKAATLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYLNSTFNP	298
QY	301	MYAFYFPWFRKALXWMLFGKIFQKDSRSCKLFL	334
DB	299	MYAFYFPWFRKALXWMLFGKIFQKDSRSCKLFL	332

RESULT 15
 US-09-782-974C-64
 Sequence 64, Application US/09782974C
 Publication No. US20030082534A1
 GENERAL INFORMATION:
 APPLICANT: Vogel, Gabriel
 APPLICANT: Lind, Peter
 APPLICANT: Wood, Linda S.
 APPLICANT: Parodi, Luis A.
 TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
 FILE REFERENCE: 41USPRM311
 CURRENT APPLICATION NUMBER: US/09/782,974C
 CURRENT FILING DATE: 2002-09-04
 PRIOR APPLICATION NUMBER: 60/165,838
 PRIOR FILING DATE: 1999-11-16
 PRIOR APPLICATION NUMBER: 09/714,449
 PRIOR FILING DATE: 2000-11-16
 PRIOR APPLICATION NUMBER: 60/198,568
 PRIOR FILING DATE: 2000-04-20
 PRIOR APPLICATION NUMBER: 60/166,071
 PRIOR FILING DATE: 1999-11-17
 PRIOR APPLICATION NUMBER: 60/166,678
 PRIOR FILING DATE: 1999-11-19
 PRIOR APPLICATION NUMBER: 60/173,396
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: 60/184,129
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: 60/185,421
 PRIOR FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: 60/185,554
 PRIOR FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: 60/186,530
 PRIOR FILING DATE: 2000-03-02
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 192
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 64
 LENGTH: 238
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-782-974C-64

Query Match 67.0%; Score 1207; DB 10; Length 238;
 Best Local Similarity 100.0%; Pred. No. 4.1e-102;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFQKQHTPTNWL	60
DB	11	MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFQKQHTPTNWL	70
QY	61	IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASIFHLFSISDR	120

Db 71 IHSMATVDFLLGCLVMPYSWPSAEHCWYFGEVFCCKIHTSTDIMLSSASIFHLSPISDR 130
Qy 121 YYAVCDPLRYKAKMNLVICVMIFISWSVPVAFPMIFLELNFKAEEIYYKHVHCRGG 180
Db 131 YYAVCDPLRYKAKMNLVICVMIFISWSVPVAFPMIFLELNFKAEEIYYKHVHCRGG 190
Qy 181 CSVFESKISGVLTFMTSFYIPGSIMLCVYRIYLIKEQARLISDANQ 228
Db 191 CSVFESKISGVLTFMTSFYIPGSIMLCVYRIYLIKEQARLISDANQ 238

Search completed: October 8, 2004, 10:31:00
Job time : 132 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2004, 10:17:10 ; Search time 19 Seconds
(without alignments)
1711.197 Million cell updates/sec

Title: US-09-633-145-2

Perfect score: 1801

Sequence: 1 MPFCHNIINISCVKNWNSD.....FGKIFQDSSRCKLFLELSS 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	677.5	37.6	337	2 JC5832	neurotransmitter r
2	529	29.4	387	2 S55550	5-HT4S receptor -
3	529	28.4	406	2 S55549	serotonin 4 recep
4	510.5	28.3	459	2 A56849	dopamine receptor-
5	497.5	27.6	465	2 I51661	dopamine D1C recep
6	493.5	27.4	363	2 I50475	dopamine D1 recep
7	486	27.0	358	2 J01278	histamine H2 recep
8	482	26.8	444	2 C55886	dopamine receptor
9	482	26.8	450	2 A55886	dopamine receptor
10	481	26.7	457	2 I51660	dopamine D1B recep
11	480	26.7	451	2 I51659	dopamine D1A recep
12	475	26.4	377	2 S68423	serotonin receptor
13	474	26.3	377	2 A53279	serotonin receptor
14	473	26.3	374	2 I77467	serotonin receptor
15	472.5	26.2	359	2 JH0449	serotonin receptor
16	467	25.9	446	2 I47217	histamine H2 recep
17	466.5	25.9	377	2 B30341	dopamine receptor
18	466.5	25.9	386	2 B72168	G protein-coupled
19	462.5	25.7	463	2 S56849	dopamine receptor-
20	461	25.6	483	2 A25896	dopamine receptor-
21	459.5	25.5	359	2 JH0449	beta-adrenergic re
22	458	25.4	446	1 DXHUD1	histamine H2 recep
23	454.5	25.2	477	1 DYHUD5	dopamine receptor
24	452	25.1	418	1 QRHYB2	dopamine receptor
25	451	25.0	418	2 S10855	beta-2-adrenergic
26	450.5	25.0	359	2 A39008	histamine H2 recep
27	450	25.0	475	2 A41271	dopamine receptor
28	449.5	25.0	464	2 S12591	beta-1-adrenergic
29	449	24.9	418	2 S00260	beta-2-adrenergic

30	446.5	24.8	415	2 I53040	beta-2 adrenergic
31	446.5	24.8	487	1 DYRTD1	dopamine receptor
32	446	24.8	466	2 Q36794	beta-1-adrenergic
33	438.5	24.3	413	1 QRHUB2	beta-2-adrenergic
34	437.5	24.3	486	2 B55886	dopamine receptor
35	433.5	24.1	477	1 QRHUB1	beta-1-adrenergic
36	432.5	24.0	366	2 A47321	serotonin receptor
37	429.5	23.8	428	2 A55044	beta-4C-adrenergic
38	429	23.8	480	2 I53053	beta 1 adrenergic
39	427.5	23.7	366	2 A26048	serotonin receptor
40	427.5	23.7	386	2 A42688	serotonin receptor
41	427.5	23.7	386	2 S18637	serotonin receptor
42	427	23.7	477	2 S71323	alpha-1A adrenergi
43	425.5	23.6	429	2 S65656	alpha-1C-adrenergi
44	425.5	23.6	466	2 JN0765	alpha-1C-adrenergi
45	425.5	23.6	499	2 S65657	alpha-1C-adrenergi

ALIGNMENTS

RESULT 1

JC5832

neurotransmitter receptor - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 24-Nov-1999

C:Accession: JC5832

R:Zeng, Z.; Fan, P.; Rand, E.; Kyaw, H.; Su, K.; Madike, V.; Carter, K.C.; Li, Y.

Biochem. Biophys. Res. Commun. 242, 575-578, 1998

A:Title: Cloning of a putative human neurotransmitter receptor expressed in skeletal mus

A:Reference number: JC5832; MUID:98125534; PMID:9464258

A:Accession: JC5832

A:Molecule type: mRNA

A:Residues: 1-337 <ZENS>

A:Cross-references: GB:AF021818; NID:G2465431; PIDN:AAC39581.1; PID:G2465432

A:Experimental source: brain

C:Genetics:

A:Map position: 6q23

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; receptor; transmembrane protein

F:29-63/Domain: transmembrane #status predicted <TM1>

F:69-95/Domain: transmembrane #status predicted <TM2>

F:114-118/Domain: transmembrane #status predicted <TM3>

F:149-173/Domain: transmembrane #status predicted <TM4>

F:186-200/Domain: transmembrane #status predicted <TM5>

F:204-229/Domain: transmembrane #status predicted <TM6>

F:253-310/Domain: transmembrane #status predicted <TM7>

F:21/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.6%; Score 677.5; DB 2; Length 337;

Best Local Similarity 39.0%; Pred. No. 3.2e-49;

Matches 130; Conservative 67; Mismatches 125; Indels 11; Gaps 4;

QY	3	FCHNIINISCVKNWNSDVRASLYSLMWLIITLTVGNLIVIVISHSFKQLHTPTNWLH	62
Db	16	FCYQ-VNGSCRTVHTLGIQLVILTCAGMLIIVLGNVFAVAFVSKALHTPTNLLL	74
QY	63	SMATVDFLLGCLVMPYSMVRSAEHCWYGEVFCIKHTSTIMLSSASIFHLSFIDRY	122
Db	75	SLALADMFLLGLVPLSTIRSVESCWPFQDFLCRLHTVLDTLFCLTSIFHLCFISIDRHC	134
QY	123	AVCDPLRYKAKNNILVICVMIFSNVDAVAFGMIFELNFKGAEEIYYKHVHCRGGS	182
Db	135	AIQDPLLYPSRFTVRVALRYILAGMGVPAAYTSFLYTDVVVETRLSQ-WLEEMPCVGSQ	193
QY	183	VFFSKISGLVTFMTSFYIPGSGIMLCVYVRIYLIKEQARLISDANKLIQIGLEKNGISQ	242
Db	194	LLLKNFQWLNFP-PLFFVPCILINISLVKVI FVATROAQQTITLSKSL-----AGAA	244
QY	243	SKERAKVKTGLVGMVFLICWCPFFICTWMDPFLHYIIPPTINDVLIWFGYINSTFPMV	302
Db	245	KHERKAATKLGIVGVILLCLWLPFTIDTMDVSLHFFITPPLVDFDIFWFAFNSACNPII	304

QY 303 YAFFPWRKALKWMLFGKIFOKDSRCKLFLE 335
 Db 305 YVFQWFRKALKLTSQKVPQTRTVDLVQOE 337

RESULT 2
 S5550
 5-HT4S receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999
 C:Accession: S5550
 R:Gerald, C.; Adham, N.; Kao, H.T.; Olsen, M.A.; Laz, T.M.; Schechter, L.E.; Bard, J.A.;
 EMBO J. 14, 2806-2815, 1995
 A:Title: The 5-HT(4) receptor: molecular cloning and pharmacological characterization of
 A:Reference number: S55549; MUID:95317299; PMID:7796807
 A:Accession: S5550
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-387 <GER>
 A:Cross-references: GB:U20906; NID:924638; PIDN:AAC52232.1; PID:g924639
 C:Superfamily: vertebrate rhodopsin

Query Match 29.4%; Score 529; DB 2; Length 387;
 Best Local Similarity 35.4%; Pred. No. 9.4e-37;
 Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

QY 25 LYSMLVLIITLVGNLIVIVISISHFQKQLH-TPTNWLHSMATVDFLLGCLVMPYMSVRS 83
 Db 22 LUTFFAMVILMAILGNLLVMVAVCDRLKRTKTYFVLSLAFADLLVSLVNAFGAIEL 81
 QY 84 AEHCWYFGEVFCIKHTSDIMLSSASIFHLSPISIDRYAV-CDPLRYKAKNILLVICVM 142
 Db 82 VQDIWYFGEVFCIKHTSDIMLSSASIFHLSPISIDRYAV-CDPLRYKAKNILLVICVM 141
 QY 143 IFISNSVPAVAFAGMIFLELNFKAEEIY---YKHVHCRGCGSVFFSKISGVLFTMTSF 198
 Db 142 LGCCWVIFPFISFLPIMOGNNIGIVDIEKRFNHNSTFCVFWNKPAYAITCSVAF 201
 QY 199 YIPGSIMLCVYRYIYLIAKEQARLISDANQKLIQIGLEMKNGISQSK----- 244
 Db 202 YIPFLMLVLYRYIYVTAKEHA-----QQIQM-LQAGATSESRPQADQHSRMT 253
 QY 245 EKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVLSNFTFPMVYA 304
 Db 254 ETKAAKTLGVINGCFCFCWAPFVTVNIDVDFIDYVPEKVTAFMLWGLVINGSLNPLFYA 313
 QY 305 FYPWFRKALKWML 318
 Db 314 FLNKSFRRAFLIIL 327

RESULT 3
 S55549
 serotonin 4 receptor - rat
 N:Alternate names: 5-HT receptor 4L
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Nov-1999
 C:Accession: S55549; S66494
 R:Gerald, C.; Adham, N.; Kao, H.T.; Olsen, M.A.; Laz, T.M.; Schechter, L.E.; Bard, J.A.;
 EMBO J. 14, 2806-2815, 1995
 A:Title: The 5-HT(4) receptor: molecular cloning and pharmacological characterization of
 A:Reference number: S55549; MUID:95317299; PMID:7796807
 A:Accession: S55549
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-406 <GER>
 A:Cross-references: GB:U20907; NID:924640; PIDN:AAC52233.1; PID:g924641
 FEBS Lett. 370, 215-221, 1995
 R:Ullmar, C.; Schmuck, K.; Kalkman, H.O.; Luebbert, H.
 A:Title: Expression of serotonin receptor mRNAs in blood vessels.
 A:Reference number: S66487; MUID:95385798; PMID:7656980
 A:Accession: S66494
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 95-259 <ULL>
 A:Cross-references: EMBL:Z48153; NID:984171; PIDN:CAA88170.1; PID:g984172
 A:Experimental source: tissue brain
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 29.4%; Score 529; DB 2; Length 406;
 Best Local Similarity 35.4%; Pred. No. 9.9e-37;
 Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

QY 25 LYSMLVLIITLVGNLIVIVISISHFQKQLH-TPTNWLHSMATVDFLLGCLVMPYMSVRS 83
 Db 22 LUTFFAMVILMAILGNLLVMVAVCDRLKRTKTYFVLSLAFADLLVSLVNAFGAIEL 81
 QY 84 AEHCWYFGEVFCIKHTSDIMLSSASIFHLSPISIDRYAV-CDPLRYKAKNILLVICVM 142
 Db 82 VQDIWYFGEVFCIKHTSDIMLSSASIFHLSPISIDRYAV-CDPLRYKAKNILLVICVM 141
 QY 143 IFISNSVPAVAFAGMIFLELNFKAEEIY---YKHVHCRGCGSVFFSKISGVLFTMTSF 198
 Db 142 LGCCWVIFPFISFLPIMOGNNIGIVDIEKRFNHNSTFCVFWNKPAYAITCSVAF 201
 QY 199 YIPGSIMLCVYRYIYLIAKEQARLISDANQKLIQIGLEMKNGISQSK----- 244
 Db 202 YIPFLMLVLYRYIYVTAKEHA-----QQIQM-LQAGATSESRPQADQHSRMT 253
 QY 245 EKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVLSNFTFPMVYA 304
 Db 254 ETKAAKTLGVINGCFCFCWAPFVTVNIDVDFIDYVPEKVTAFMLWGLVINGSLNPLFYA 313
 QY 305 FYPWFRKALKWML 318
 Db 314 FLNKSFRRAFLIIL 327

RESULT 4
 A56849
 dopamine receptor-like protein D14 - Japanese pufferfish
 C:Species: Fugu rubripes (Japanese pufferfish)
 C:Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
 C:Accession: A56849
 R:Macrae, A.D.; Brenner, S.
 Genomics 25, 436-446, 1995
 A:Title: Analysis of the dopamine receptor family in the compact genome of the puffer fi
 A:Reference number: A56849; MUID:95309911; PMID:7789977
 A:Accession: A56849
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-459 <MAC>
 A:Cross-references: GB:X80174; NID:g1204089; PIDN:CAA56455.1; PID:g1204090
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 28.3%; Score 510.5; DB 2; Length 459;
 Best Local Similarity 37.0%; Pred. No. 3.9e-35;
 Matches 118; Conservative 54; Mismatches 110; Indels 37; Gaps 8;

QY 31 LIILTLVGNLIVIVISISHFQKQLHT-TNWLHSMATVDFLLGCLVMPYMSVRSABHCWY 89
 Db 32 LIILTLVGNLIVIVISISHFQKQLHT-TNWLHSMATVDFLLGCLVMPYMSVRSABHCWY 91
 QY 90 FGEVFCIKHTSDIMLSSASIFHLSPISIDRYAVCDPLRYKAKNILLVICVMIFTSV 149
 Db 92 FGE-FCNIWVAFDIMGCTASILNLCVISVDRIWAISSPPRYEKMTKPKVACLMSVAVWL 150
 QY 150 PAVFAGMIFLELNFKAEEIYKHVHCRG-----GCSVFFSKISGVLFTMTSFYI 200
 Db 151 SVLISF--IPVQLNWHKAQTASY--VELNGTVAGDLPDNCDSLLNRTVAISSLSIFYI 206
 QY 201 PGSIMLCVYRYIYLIAKEQARLI-----SDANQKLIQIGLEMKNGISQSKER 246
 Db 207 PVAIMIVTYTRYIAQKQIRIRISALERAESAQNHRHSSMGNSLSESCSFKMSFKRET 266

QY 247 KAVKTLGIVMGVFLICWCPEFFICTVMDPFLHY-----LIPTLNDVLWFGYLNSTFN 299
Db 267 KVLKTLVIMGVFVCCWLPFFILNCMVFPCEADDTTDFPCISSTTDFVFWFGWANSLSL 326
QY 300 PMVYAFYFVFWFRKALKOML 318
Db 327 PIYAFNAD-FRKAFFSILL 344

RESULT 5
151661
dopamine D1c receptor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I51661
R:Sugamori, K.S.; Demchishyn, L.L.; Chung, M.H.; Niznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A:Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: I51659; MUID:95024150; PMID:7937989
A:Accession: I51661
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-465 <SUG>
A:CROSS-references: EMBL:U07865; NID:g559763; PIDN:AAA50830.1; PID:g559764
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 27.6%; Score 497.5; DB 2; Length 465;
Best Local Similarity 34.5%; Pred. No. 4.8e-34;
Matches 118; Conservative 61; Mismatches 130; Indels 33; Gaps 8;

QY 6 NIINISCVKNWNSD-----VRASLYSLMWLIILTLVGNLIVIVISHFQKLTHTP 56
Db 5 SIPNVTV---NVWHDLDVGNDSLRLTGLLLSLTLTGNTLVCLAVTKFRHLRSK 62

QY 57 -TNWLIHSMATVDFILGCLVMPYSVMSAEHCWYFGEVFKIHTSTDIMLSSASIFHLGSF 115
Db 63 VTNFFVISLAVSDLFVALLVMPKATEVAGFWFGD-FCDTWAFDINCMSTASILNLCI 121

QY 116 ISIDRYAVCDPLRYKAKKNILVICVMIFISVPAVAFPMIFLELNFKGAEIYKHYH 175
Db 122 ISLDRYWALASPFRYERKMTQVAFIMIGVAMTSLISFIPQLSWHKSHEADBELNGV 181

QY 176 HCRGCSVFFSKISGLVLTWMTSYIPGSMTCVYRIYLAKQEARLISDAN-----OK 229
Db 182 NHTENCDSLNRTYALISSLSISFYIPVIMIGTYRIYIAQTQIRRISSLERAVERHAQR 241

QY 230 LOIGLEMKNGISQS--KERKAVKTLGIVMGVFLICWCPEFFICTVMDPFLHYIIP----- 281
Db 242 CSSRLSNENSLKTSFRKETKVLKTLISINGVVFVFWLFFVLNCLMIPFCHMLPGQNEPE 301

QY 282 -----PTLNDVLWFGYLNSTNPMVYAFYFVFWFRKALKOML 318
Db 302 PPCVSETTNIWFVFGWANSLSNPNVIYAFNAD-FRKAFTTIL 342

RESULT 6
150475
dopamine D1 receptor - goldfish
C:Species: Carassius auratus (goldfish)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I50475
R:Frail, D.E.; Manelli, A.M.; Witte, D.G.; Lin, C.W.; Steffey, M.E.; Mackenzie, R.G.
Mol. Pharmacol. 44, 1113-1118, 1993
A:Title: Cloning and characterization of a truncated dopamine D1 receptor from goldfish
A:Reference number: I50475; MUID:94088471; PMID:8264547
A:Accession: I50475
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-363 <FRA>
A:CROSS-references: GB:L08602; NID:g212949; PIDN:AAA16322.1; PID:g212950
C:Superfamily: vertebrate rhodopsin

C:Keywords: neurotransmitter receptor

Query Match 27.4%; Score 493.5; DB 2; Length 363;
Best Local Similarity 36.3%; Pred. No. 8.2e-34;
Matches 118; Conservative 59; Mismatches 117; Indels 31; Gaps 8;

QY 21 VRASLYSLMWLIILTLVGNLIVIVISHFQKLTHTP-TNWLHSMATVDFILGCLVMPYS 79
Db 23 VRVLTGCFSLVILSLTGLNTLVCAATKFRHLRSKVTNFFVISLAVSDLLVAVLWPMK 82

QY 80 MVSRAEHCWYFGEVFKIHTSTDIMLSSASIFHLSPISIDRYAVCDPLRYKAKKNILVI 139
Db 83 ATEVAGFWPFG-AFCDIWAFFDINCMSTASILNCLVISVDRYWAISSPRYEKMTPRVA 141

QY 140 CVMIFISVPAVAFPMIFLELNFKGAEIYKHYHVC-----RGCSVFFSKISGLVLT 193
Db 142 FVMISGAWTSLVLSIF--IPVLKWHKAQPIGFLVNASRRDLPTDNCSSLNRTYAISS 199

QY 194 FMTSFYIPGSMICVYRIYLIAKQEARLIS--DANQKLQI-----GLEMKNG 239
Db 200 SLISFYIPVAIMIVTQIYRIAQIRISALERAESAQIRHDSMGSGSNMDESSPK 259

QY 240 ISQSKERKAVKTLGIVMGVFLICWCPEFFICTVMDPFLHY-----IIPTLNDVLWFGY 293
Db 260 LSPKRETKVLKTLVIMGVFVCCWLPFFILNCMVFPCKTSNGLPCISPTTDFVFWFGW 319

QY 294 LNSTNPMVYAFYFVFWFRKALKOML 318
Db 320 ANSSLNPIIYAFNAD-FRFAFILL 343

RESULT 7

QY1278
histamine H2 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C:Accession: JQ1278
R:Ruot, M.; Traiffort, E.; Arrang, J.M.; Leurs, R.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 179, 1470-1478, 1991
A:Title: Cloning and tissue expression of a rat histamine H2-receptor gene.
A:Reference number: JQ1278; MUID:92028990; PMID:1930188
A:Accession: JQ1278
A:Molecule type: DNA
A:Residues: 1-358 <RUA>
A:CROSS-references: GB:S57565; NID:g236183; PIDN:AAB19935.1; PID:g236184
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:22-45/Domain: transmembrane #status predicted <TM1>
F:58-81/Domain: transmembrane #status predicted <TM2>
F:93-113/Domain: transmembrane #status predicted <TM3>
F:136-159/Domain: transmembrane #status predicted <TM4>
F:178-203/Domain: transmembrane #status predicted <TM5>
F:234-260/Domain: transmembrane #status predicted <TM6>
F:267-288/Domain: transmembrane #status predicted <TM7>
F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:220,311,315/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 27.0%; Score 486; DB 2; Length 358;
Best Local Similarity 34.0%; Pred. No. 3.4e-33;
Matches 117; Conservative 56; Mismatches 123; Indels 48; Gaps 7;

QY 11 SCVKKNWSDVPRASLYSLMWLIILTLVGNLIVIVISHFQKLTHTP-TNWLHSMATVDFL 70
Db 9 SCCLDSMALKVTISV--VLTTLITITAGVNVVCLAVSLNRLRLSLTNCFVSLAATDIL 66

QY 71 LGCLVMPYSVMSRAEHCWYFGEVFKIHTSTDIMLSSASIFHLSPISIDRYAVCDPLRY 130
Db 67 LGLLVLPFSAIYQLSFTWSFGVFCNIYITSLDMLCTASILNLFMSIDORYCAVTDPLRY 126

QY 131 KAKMNLIVCMIFISVPAVAFPMIFLELNFKGAEIYKHYHVC-----CSVFF 185
Db 127 PVLVTPVRVAISLVFIWISITLSLSFLSHLGWNSRG-----TRGNDTFCKKQV 177


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QY 251 TLGIWGVFLICWCPFFICTVMDPFLHY-----IIPPTLNDVLIWFGYLNSTENP 300
Db 283 TLISINGVFCWCLWPPFIILNCWVFCDSRGHQPAGLPCVSETTFDIFWFGWANSLLNP 342
QY 301 MYVAFYPMFRKALKMML 318
Db 343 ILYAFNAD-FRKVFSSLL 359

RESULT 11
151659
dopamine D1A receptor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I51659
R:Sugamori, K.S.; Demchyshyn, L.L.; Chung, M.H.; Niznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A:Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: I51659; MUID:95024150; PMID:7937989
A:Accession: I51659
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-451 <RUG>
A:Cross-references: EMBL:U07863; NID:g559759; PIDN:AAA50828.1; PID:g559760
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 26.7%; Score 480; DB 2; Length 451;
Best Local Similarity 34.5%; Pred. No. 1.4e-32;
Matches 111; Conservative 56; Mismatches 117; Indels 38; Gaps 7;

QY 31 LLIILTLVGNLIVIVISHFVKOLHTP-TNWLHSMATVDLGLVMPYSMVRSAEHCWY 89
Db 31 VLIILTLGNTLVCAVIRFRLRSKVTNFFVLSLAVSDLLVAVLWPKVAEITAGFWP 90
QY 90 FGEVFCIKHTSDIMLSSASIFHLSFISIDRYAVCDPLRYKAKMNLIVCMIFISWSV 149
Db 91 FG-TECNIWAFDMCSTASILNLCVISVDRYWAISPPFYEKMTKTPKVAFTMIGAWTL 149
QY 150 PAVFAFGMFLFELNFKGAEIYY-----KHVHRCGGCVSFFSKISGVLTFTMTSPYIP 203
Db 150 SVLISF-IPVQLNWHKATTSFFDLNLTHTDMNCDSLNRTVAISSLSISFYIPVA 207
QY 204 IMLCVYRYLYLAKQARLISDANKQLQIGLEMKGISQ-----SKER 246
Db 208 IMVITYRYRAAKQIRISALERAHVAKNCONSTNRNSLDCQOPSSSLKTSFKRET 267
QY 247 KAVKTLGIWGVFLICWCPFFICTVMDPFLH-----YIIPPTLNDVLIWFGYLYNS 296
Db 268 KVLKTLGVIMGVFCWCLWPPFIILNCVPCDPSLITSGTEPFCISSTTFDVFVFWGANS 327
QY 297 TPNVMVYAFYPMFRKALKMML 318
Db 328 SLNPIIYAFNAD-FRKAFSNLL 348

RESULT 12
568423
serotonin receptor 1D alpha - rabbit
N:Alternate names: 5-hydroxytryptamine receptor 1D alpha (5-HT1Dalpha)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S68423
R:Harwood, G.; Lockyer, M.; Giles, H.; Fairweather, N.
FEBS Lett. 377, 73-76, 1995
A:Title: Cloning and characterisation of the rabbit 5-HT (1D-alpha) and 5-HT (1D-beta) receptors.
A:Reference number: S68422; MUID:96130324; PMID:8543023
A:Accession: S68423
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-377 <HAR>
A:Cross-references: EMBL:Z50162; NID:g1004281; PIDN:CAA90530.1; PID:g1004282
C:Superfamily: octopamine receptor type I
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C:Keywords: neurotransmitter receptor

Query Match 26.4%; Score 475; DB 2; Length 377;
Best Local Similarity 32.0%; Pred. No. 3e-32;
Matches 112; Conservative 62; Mismatches 120; Indels 56; Gaps 7;

QY 21 VRASLYSLMVLILTLVGNLIVIVISHFVKOLHTP-TNWLHSMATVDLGLCLVMPYSM 80
Db 37 LKISLAVLSVITLAVLSNAPVLTLLTRKLHTPANYLIGSLATDLLVSLVMPISI 96

QY 81 VRSAEHCWYFGEVFCIKHTSDIMLSSASIFHLSFISIDRYAVCDPLRYKAKMNLIVIC 140
Db 97 AVTITHWNFGQVLCDIWSSDITCTASILHLCVIALDRYWAITDALEYSKERTAGHAA 156

QY 141 VMFISWSVPVAFAGMIFLELNFKGAEIYYKHVHRCGGCVSFFSKIS-GVLTFTMTSPY 199
Db 157 AMIAVVAISICISIPPLFWR-QAKAHEV-----SDCLVNTSQISYTIYSTCGAFY 207

QY 200 IFGSIMLCVYRYLYIAKEQ-----ARLISDA----- 226
Db 208 IPSVLLIIVLYGRIYMAARNRILNPPSLYGKRRTTAHLITGSAGSSLCSLPSLGEHSHS 267

QY 227 -----NOKLQIGLEMKNGISQSKERKAVKTLGIWGVFLICWCPFFICTVMDPFL 276
Db 268 AGSPLEFNPVRIKLADSVLERKRIISAARERKATKTLGIILGAFICGWLPPFFVASLVLPIC 327

QY 277 H--YIIPPTLNDVLIWFGYLYNSTFPMVYAFYPMFRKALKMML-FGKIP 323
Db 328 RDSWMPGLEDFFTWLGYLNSLINPIIYTVFNEDFRQAFORVIHFRKAF 377

RESULT 13

AS3279

N:Alternate names: 5-hydroxytryptamine receptor 1D (5-HT1D); 5HT-1D alpha receptor

C:Species: Homo sapiens (man)

C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 05-Nov-1999

C:Accession: A53279; A4136

R:Hamblin, M.W.; Metcalf, M.A.

Mol. Pharmacol. 40, 143-148, 1991

A:Title: Primary structure and functional characterization of a human 5-HT-1D-type serot

A:Reference number: A53279; MUID:91342595; PMID:1652050

A:Accession: A53279

A:Molecule type: DNA

A:Residues: 1-377 <HAM>

A:Cross-references: GB:M89955; NID:g177771; PIDN:AAA35491.1; PID:g177772

R:Weinshank, R.L.; Zgombick, J.M.; Macchi, M.J.; Branchek, T.A.; Hartig, P.R.

Proc. Natl. Acad. Sci. U.S.A. 89, 3630-3634, 1992

A:Title: Human serotonin 1D receptor is encoded by a subfamily of two distinct genes: 5-

A:Reference number: A44136; MUID:92228840; PMID:1565658

A:Accession: A44136

A:Molecule type: mRNA

A:Residues: 1-377 <WEI>

A:Cross-references: GB:M81589; NID:g338023; PIDN:AAA60315.1; PID:g338024

C:Genetics:

A:Gene: GDB:HTR1D

A:Cross-references: GDB:132416; OMIM:182133

A:Map position: lp36.3-lp34.3

A:Introns: #status absent

C:Superfamily: octopamine receptor type I

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme

Query Match 26.3%; Score 474; DB 2; Length 377;
Best Local Similarity 33.3%; Pred. No. 3.6e-32;
Matches 120; Conservative 57; Mismatches 111; Indels 72; Gaps 11;

QY 21 VRASLYSLMVLILTLVGNLIVIVISHFVKOLHTP-TNWLHSMATVDLGLCLVMPYSM 80
Db 37 LKISLAVLSVITLAVLSNAPVLTLLTRKLHTPANYLIGSLATDLLVSLVMPISI 96

QY 81 VRSAEHCWYFGEVFCIKHTSDIMLSSASIFHLSFISIDRYAVCDPLRYKAKMNLIVIC 140
Db 97 AVTITHWNFGQVLCDIWSSDITCTASILHLCVIALDRYWAITDALEYSKERTAGHAA 156

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Qy 141 VMIFSNVPAVFAGMIFLEINPKGAEIYYKXVHCRGGCVFESKIS-GVLTFMTGTFY 199
Db 157 TMIAIVMAISICISIPPLFWR-QAKAQOBEM-----SDCLVNTSQISYTIYSTCGAFY 207
Qy 200 IPGSTMLCVYRYVLIAREQ-----ARLIJSDA-----NQKLOIG----- 233
Db 208 IPSVLLIILYGRIVYRAARNRIINPPSLYKGRFTTAHLITGSAGSLCSLNSSLHGHSHS 267
Qy 234 -----LEMKNGISQSOKERKAVKTLGIIVMGVFLICWCFFPFICTVMDP- 274
Db 268 AGSPULFFNHVKIKLADSALERK-ISAARERKATKILGIILGAFIICMLPFFVSVSLVLP 326
Qy 275 -----FLHYIIPPTINDVLVIFGYLNTFNPMVYAFFYFWRPKALKOMMLFGKI--FQKDS 327
Db 327 CRDSCWIIH-----PALFDFTLGYLNSLINPIIYTVFNEEPRQA-----FOKIVFPRKAS 377

RESULT 14
177467
serotonin receptor 1D - rat
N:Alternate names: 5-hydroxytryptamine receptor 1D (5-HT1RD)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999
C:Accession: I77467

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C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Nov-1999
C:Accession: JH0449; I52319
R:Gantz, I.; Munzert, G.; Tashiro, T.; Schaeffer, M.; Wang, L.; Delvalle, J.; Biochem. Biophys. Res. Commun. 178, 1386-1392, 1991
A:Title: Molecular cloning of the human histamine H2 receptor.
A:Reference number: JH0449; MUID:91337087; PMID:1714721
A:Accession: JH0449
A:Molecule type: DNA
A:Residues: 1-359 <G>
A:Cross-references: GR:M64799; NID:G184087; PIDN:AAA58647.1; PID:G184088
R:Nishi, T.; Koike, T.; Oka, T.; Maeda, M.; Futai, M. Biochem. Biophys. Res. Commun. 210, 616-623, 1995
A:Title: Identification of the promoter region of the human histamine H2 receptor.
A:Reference number: I52319; MUID:95275518; PMID:7755641
A:Accession: I52319
A>Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <R>
A:Cross-references: GR:D49783; NID:G728495; PIDN:BAA08618.1; PID:G728496
C:Comment: Histamine is important in the regulation of gastric acid secretion.